## November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_New).

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Sequence 3439, Ap Sequence 3966, Ap Sequence 171, App Sequence 495, App Sequence 45240, A Sequence 185, App Sequence 115, App Sequence 11, App Sequence 30, Appl Sequence 30, Appl

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Sequence 52875, A Sequence 52875, A Sequence 30691, A Sequence 30691, A Sequence 49778, A Sequence 49778, A Sequence 49778, A

Sequence 42931,

Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

Minimum DB Maximum DB

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AlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMetThrLeuAspVal 24
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APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US,11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 3214
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US-11-025-554A-485
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US-11-121-086-13
US-10-240-708-27
US-10-240-708-27
US-10-240-708-27
US-10-240-783-626-3966
US-11-052-554A-495
US-11-052-554A-495
US-11-052-554A-495
US-11-052-554A-495
US-10-750-185-30691
US-10-750-623-42840
US-10-750-623-42840
US-10-750-185-30891
US-10-995-561-469
US-10-995-561-469
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Publication No. US20050287570A1
GENERAL INFORMATION:
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-Q=/Cgn2 1/USPTO spool/US10751235/runat 12012006 120916 2581/app_query.fasta 1.263
-DB=Published Applications NA New -QFWT=fastap -SUFFIX=p2n.mpbn -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bIts -START=1 - MATRIX=blosume2
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=10
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-NORPH=S -LOOPCH=0 -NORM -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
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Sequence 26357, A
Sequence 26357, A
Sequence 31952, A
Sequence 31952, A
Sequence 1111, Ap
Sequence 3332, Ap
Sequence 4111, Ap
                                                                                                     January 15, 2006, 13:20:20; Search time 232 Seconds (without alignments) 268.620 Million cell updates/sec
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3: /cgn2 6/ptodata/2/pubpna/USO7 NEW PUB.seq:*
4: /cgn2 6/ptodata/2/pubpna/PCT NEW PUB.seq:*
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6: /cgn2 6/ptodata/2/pubpna/USO1 NEW PUB.seq:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                             nucleic search, using frame_plus_p2n model
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US-10-750-623-31952
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Database

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Sequence 467, App Sequence 469, App Sequence 46677, A Sequence 46677, A Sequence 909, App Sequence 43888, A Sequence 43888, A Sequence 45175, A Sequence 45175, A

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Alignment Scores:
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25 IleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAspSerProValIle 44
                                                                                                                                                                                                              44 IleGluAlaValTyrThrAlaLeuLy8------GluAlaGluLeuArgSerThr 59
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                                                                                                                                          | FUDICATION NO. USZUUDUZEUGUJAI
| GENERAL INFORMATION | GENERAL INFORMATION | APPLICANT: MAI GENONICS, INC. | APPLICANT: MAIGH GENONICS, INC. | APPLICANT: MAICH RENEW RICHARD | APPLICANT: ROSENFELD, David | APPLICANT: HOLM, Tom | AFPLICANT: BATES, Stephen | AFPLICANT: BATES, Stephen | AFPLICANT: BATES, Stephen | AFPLICANT: BATES, STEPHEN | COMPOSITIONS FOR INFERRING BOVINE TRAITS | FILE REFERENCE: MMI1100-2 | GIRRENT ELING DATE: 2003-12-31 | FRICK PRICK PAIL OF STO ID NOS: 64922 | SOFTWARE PATENT VERSION NUMBER: US 60/437,482 | PRIOR PLING DATE: 2002-12-31 | NUMBER OF STO ID NOS: 64922 | SOFTWARE PATENT VERSION 3.1 | SEQ ID NO 26357 | SEQ ID NO 26357 | SEQ ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SEQ ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION NUMBER OF STO ID NO 26357 | SED INCOTATION 
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US-10-750-623-26357/C
| Sequence 26357, Application US/10750623
| Fublication No. US20050287531A1
| GENERAL INFORMATION:
| APPLICANT: NMI GENOMICS, INC.
| APPLICANT: MAI GENOMICS, INC.
| APPLICANT: KERK Richard
| APPLICANT: KERK Richard
| APPLICANT: RENEWRID. David
| APPLICANT: HOLM, TOOM
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; Sequence 26357, Application US/10750185
; Publication No. US20050260603A1
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APPLICANT: FANTIN, Dentis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-1
CURRENT PELLING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 26357
LENGTH: 3198
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
TILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US (0/437,482
PRIOR APPLICATION NUMBER: US (0/437,482
PRIOR PLING DATE: 2002-12-31
PRIOR PILING DATE: 2002-12-31
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 31952
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27.16%
16.41%
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42.59%
31.48%
17.18%
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Best Local Similarity:
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US-10-750-623-26357
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US-10-750-185-31952
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385 AAAGCAAGAGACTTTGGTGTTTCGTAGCTTTTTACAAGAAGCAAACTATATAAATCT 444
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                                                                                                                       Sequence 1611, Application US/10793626
PUBLICATION NO. US2005025478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVERTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 2004-03-04
PRIOR PILING DATE: 1999-11-09
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Sequence 3932, Application US/10793626
Sequence 3932, Application US/10793626
Sequence 3932, Application No. US20050255478A1
Publication No. US20050255478A1
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SEQ ID NOS: 4472
SEQ ID NO 3932
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1611
LENGTH: 804
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Best Local Similarity:
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67 Ile 67
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US-10-793-626-1611
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3287 GAGAAGTATAACAGAGGGGTTCTGAAATAGGAAGAGACAGCAGTTTTAGTCCACTCTAG 3228
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                                                                                                   22 LeuAspValileGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAspSer 41
                                                                                                                                                                                 42 Pro-----ValileGlu------AlaValTyrThrAlaLeuLysGluAlaGlu 55
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APPLICANT: ROSENFELD, David
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILLIOG-1
CURRENT FILING DATE: 2003-12-31
PRIOR PILLING DATE: 2002-12-31
PRIOR PILLING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE PATENTIN Version 3.1
SOFTWARE PATENTIN Version 3.1
                 2 GlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMetThr
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Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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ORGANISM: Bovine 19866880527023
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US-10-750-623-31952/c
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US-10-750-623-31952
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Sequence 484, Application US/11052554A

| Sequence 484, Application US/11052554A
| Publication NO. 22005028866A1
| CENERAL INFORMATION:
| APPLICANT: Sachdeva, et al. |
| TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN-LIKE TITLE OF INVENTION: WINDER: US/11/052,554A |
| TITLE OF INVENTION: DATE: 2005-02-07 |
| PRIOR PILING DATE: 2004-07-20 |
| PRIOR APPLICATION NUMBER: US 60/589,227 |
| PRIOR APPLICATION NUMBER: US 101/052,554A |
| CURRENT FILING DATE: 2004-07-06 |
| PRIOR APPLICATION NUMBER: US 101/052,554A |
| PRIOR APPLICATION NUMBER: US 101/052,554
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                 72 LysileValProArg
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US-11-150-888-16
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US-11-052-554A-484
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Sequence 4116, Application US/10793626

Publication No. US2005025478A1

Publication No. US2005025478A1

Publication No. US2005025478A1

APPLICANT: KIMMERLY, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT FILING DATE: 2004-03-04

PRIOR PILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4116

LENGTH: 3660
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Matches:
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Matches:
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; OTHER INFORMATION: nucleic acid sequence US-10-793-626-3932
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APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounte, William M.
APPLICANT: Mounte B.
APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Bugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYMUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OF INVENTION: NOVEL POLYMUCLEOTIDE ARRAYS
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION.
FILE REFERENCE: 01997.027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT PILLING DATE: 2005-05-11
PRIOR FILING DATE: 2004-05-11
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                                                                                                                                                      Sequence 13, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
TITLE OP INVENTION: UUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REPERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR PPLING DATE: 2004-05-04
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    301 TCTCCGGCCTATCAAGCTGTGGCTTTAGCGCTCAATGCGGCT---
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Indels:
                                                               343 ---GTGGGCATGTGGCAAGTCATAGCC 366
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Publication No. US20060003958A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.3
SEQ ID NO 13
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US-11-121-086-13/c
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853460359A
CURRENT PAPLICATION NUMBER: US/11/052,554A
CURRENT PILING DATE: 2005-02-07
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-30
PRIOR PILING DATE: 2004-02-06
SEQ ID NOS: 763
SOFTWARE: PATENTING DATE: 2004-02-06
SEQ ID NOS : 763
SOFTWARE: PATENTING DATE: 2004-02-06
LENGTH: 2091
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; Sequence 485, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; TYPE: DNA
; ORGANISM: Helicobacter pylori J99
US-11-052-554A-484
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ORGANISM: Helicobacter pylori J99
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Sequence 27, Application US/10240708
Publication No. US20050282157A1
GENERAL INFORMATION:
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITILE OF INVENTION: Dy Assessing DNA Methylation
FILE REPERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
PRIOR PAPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
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1530 CAGAAGGCCAGGAAGATTTAAAGTTTAATTTTTTAATCCCTTTATTCTCCCATAATA 1589
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1590 CTGTTTCCATTCCTTACCACAATATATGACTTGTTAAGGTTCTCCCATTTTTCCAAGACAA 1649
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                SOFTWARE: PatentIn version 3.3
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LOCATION: (481)..(501)
OTHER INFORMATION: n is a,
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LOCATION: (405)..(423)
OTHER INFORMATION: n is a,
                                                                                  ORGANISM: Cricetinae gen.
NUMBER OF SEQ ID NOS: 7285
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LOCATION: (366)...(400)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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                                SEQ ID NO 473
LENGTH: 2858
                                                                    TYPE: DNA
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Publication No. US20050255478A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: WIRBER: US/0/793,626
CURRENT APPLICATION NUMBER: US/0/193,626
CURRENT FILING DATE: 2004-03-04
PRIOR FILING DATE: 1999-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description of Artificial Sequence: synthetic nucleic acid sequence
                                                                                                                                                                    ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-240-708-27
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PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 27
LENGTH: 11131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1623
LENGTH: 1494
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COTHER INFORMATION:
US-10-793-626-1623
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Aebl6929 Barley cy
Aebl6929 Sunflower
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Aebl6930 Green alg
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Ady27356 Bacillus
Ady27458 Bacillus
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Aaf26268 B. megate
Aaf26324 B. megate
Acc48000 B. megata
Abz70676 Bacillus
Aal54548 DNA of P4
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drought tolerance; disease resistance; galactomannan production;
plant growth regulator; heat tolerance; herbicide tolerance;
lignin production; extreme osmotic condition tolerance;
pathogens resistance; pest resistance; yield improvement; seed oil yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                               AEB16925
AEB16924
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ADO81358
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AAX60780
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AEB16947
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ADY27460
ADY27469
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ABK74941
AASO2937
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ADY27456
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AAD02365
AAF54832
AAF26268
AAF26324
ACC48000
ABZ70676
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28-APR-2003; 2003US-00425115.
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 Command line parameters:
-MODEL=frame+ pin.model -DEV=xlh
-MODEL=frame+ pin.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10751235/runat_12012006_120915_2508/app_query.fasta_1.263
-Q=/cgn2_1/USPTO_spool/US10751235/runat_12012006_120915_2508/app_query.fasta_1.263
-DB=N Geneseq -QEMT=fastap -SUFFIX=pin.ring -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bite -START=1 -RND=-1 -MATRIX=blosum62 -FRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=per -THR MAX=100 -THR MINEN O -ALIGN=150 -MODE=LOCAL
-UTFRT=ptc -NORM=ext -HEAPSIZE=560 -MINLEN=0 -MAXLEN=200000000
-USER=US10751235_@CGN 1 1 727 @runat_12012006_120915_2508 -NCPU=6 -ICPU=3
-NOWANP -LARGEQUERY -NGG SCORES=0 -WALT -NORM=CK=100 -LONGIAG
-DBV TIMBGUT=120 -WARN TIMEOUT=30 -THRADS=1 -XGARPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DBLEXT=7
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Aeb16909 Thale cre
Aeb16911 Thale cre
Aeb16910 Thale cre
                                                                              January 15, 2006, 05:07:45 ; Search time 474 Seconds (without alignments) 1082.661 Million cell updates/sec
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                                                                                                                                            393
1 LQPYAEDGSAVNMEAKFSQM.....STDLLPYWKIDALCKIVPRQ
            5.1.6
Compugen Ltd
                                                          nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                         4996997 seqs, 3332346308 residues
           GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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Database :

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Score

Result Š.

(KOVA/) KOVALIC D K.

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The invention relates a recombinant DNA construct comprising a polypeptide with any of 5544 amino acids sequences (CDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The CDNAs and proteins are from corn, soybean, (SEQ ID NO: 5545-11088). The CDNAs and proteins are from corn, soybean, captured and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising transformed complexity is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased cresistance to plant disease, for galactomannan production, for production of plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to extreme osmotic conditions, for improvement by colditication of carbohydrate, in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improvement by colditication of carbohydrate, introgen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may calso encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and conditions plant tolerance to blooding increasing plants with improved plant tolerance to blooding increasing plants with improved plant tolerance to blooding increasing plante tolerance to blooding increased processed increased planted and for pro
                                                                                                                               New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analysis systems. The present sequence is one of the 5544 plant CDNA sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerProvalileGluAlavalTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
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gene] cDNA. Note: The current sequence
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                                                                                                                                                                                                      Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97C1; cytochrome P450 97C1; gene; ss; chromosome 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific
(pos:496...650, aa:Thr-Ala)
(pos:942...1037, aa:Lys-Ile)
(pos:1242...1326, aa:Val-Ser)
(pos:1420...1523, aa:Lys-Asn)
(pos:1662...1841, aa:Val-Leu)
(pos:1089...2005, aa:Val-Trp)
(pos:2081...2183, aa:Lys-Phe)
(pos:2240...2440, aa:Asn-Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2467 BP; 657 A; 491 C; 521 G; 798 T; 0 U; 0 Other;
                                                                                                                                                                            Thale cress LUT1 (cytochrome P450 97C1) cDNA, SEQ ID NO: 5.
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986 GAACAATTGGATTCTTGTTAATTGAGAGGTTTGGTTGTTTTTTTCAGATCGATGCATTG 1045
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                                                                                                                                     ThrLeuAspValIleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrAsp 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   engineering; antioxidant; transgenic plant; CYP97C1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific
                                                                                                 SerProvalileGluAlavalTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
                                                                                                                                                      807 ACACTIGATGTCATIGGGTIGTCTTTTTTAACTACAATTTCGATTCTTTGACTACTGAT
                                                                                LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
                                                                                                                                                                                                                                               LeuLeuProTyrTrpLyalle------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thale cress mutant LUT1 (cytochrome P450 97C1) cDNA, SEQ ID NO: 7.
    131
Mismatches:
Indels:
Gaps:
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(KIMJ/) KIM J.
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986 GAACAATTGGATTCTTGTTAATTGAGAGGGTTTGGTTGTTTTTTTCAGATCGATGCATTG 1045
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                                                                                                                                                                                                                                                                                                                                                                          CTTCTGCCATATTGGAAGGC-AAGTTTCCTGTGTTTTTTCTGTGGTTTGTTGATTGTGTG 985
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invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is thale cress LUT1 [cytochrome P450 monooxygenase (CYP97C1)] mutant cDNA.
                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                -----AspAlaLeu 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97C1; cytochrome P450 97C1; gene; ds; chromosome 3.
                                                                                                                                                                                                                   747 TTGCAGCCTTATGCAGAAGACGGAAGTGCTGTGAATATGGAAGCGAAGTTCTCTCAGATG
                                                                                                                                                                                                                                                  ThrLeukspValileGlyLeuSerLeuPheAsnTyrksnPheAspSerLeuThrThrAsp
                                                                                                                                                                                                                                                                                                  SerProvalileGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAp
                                                                                                                                                                                                                                                                                                                          AGTCCTGTCATTGAAGCTGTTTACACTGCTCTTAAAGAAGCTGAGCTTCGTTCTACTGAT
                                                                                                                                                                                                                                                                           ACACTTICATICICATTICGCTTICTTTTTTAACTACAATTTTCGATTCTTTTGACTACTGAT
                                                                                                                                                                                                    LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New expression vector comprising a nucleic acid sequence encoding
                                                          BP; 658 A; 491 C; 520 G; 798 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thale cress LUT1 (cytochrome P450 97C1) DNA, SEQ ID NO:
                                                                                            2467
76
0
1
31
                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                   LeuLeuProTyrTrpLysIle------
                                                                                                                                                                             x AEB16911 (1-2467)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEB16910 standard; DNA; 4170
                                                                                          7.79e-42
346.00
71.03$
71.03$
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                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                               US-10-751-235-1 (1-77)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2005150002-A1
                                                          Sequence 2467
                                                                                  Alignment Scores:
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1756 TIGCAGCCTTATGCAGAAGACGGAAGTGCTGTGAATATGGAAGCGAAGTTCTCTCAGATG 1815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1816 ACACTTGATGTCATTGGGTTGTCTCTTTTTAACTACAATTTCGATTCTTGACTACTACTAT 1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1995 GAACAATIGGATICTIGITAAIIGAGAGGGTTIGGTIGTITITITTCAGAICGAIGCAITG 2054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCTGCCATATIGGAAGGC-AAGTTTCCTGTGTTTTTTTCTGTGGTTTGTTGATTGTGTG 1994
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                                                                                           The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is thale cress LUT1 [cytochrome P450 monooxygenase (CYP97C1); A1393130 genel genomic DNA. Note: The current sequence is that of thale cress LUT1 DNA which is located on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "Maize cytochrome P450 97C (CYP97C) protein"
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97C; cytochrome P450 97C; gene; 88.
polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------AspAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGInProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLygPheSerGlnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerProvalileGluAlavalTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 ThrLeuAspVallleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
                                                                                                                                                                                                                                                                              C; 812 G; 1274 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize cytochrome P450 97C (CYP97C) cDNA, SEQ ID NO: 26
                                                                                                                                                                                                                                                                                                                                 4170
76
0
1
31
                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                     Claim 10; SEQ ID NO 6; 135pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysLysIleValProArgGln 77
|||||||||||||||||||||
TGTAAGATAGTCCCGAGACAG 2075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LeuLeuProTyrTrpLysIle----
                                                                                                                                                                                                                                                                                   Sequence 4170 BP; 1222 A; 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEB16928 standard; cDNA; 531
                                                                                                                                                                                                                                                                                                                               1.63e-41
346.00
71.03%
71.03%
88.04%
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                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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DB:
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AEB16928
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The present invention relates to genes, proteins and methods comprising carotemoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotemoid ratios in plants and microoxyanisms using LuT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotemoid production in a plant for enhancing production of specific carotemoid compounds that are potent antioxidants. The present sequence is maize cytochrome P450 monooxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ACALTGGATGGATTGGTTTATCATTGATTATGATTTTGATTCCCTCAACAGAT 120
                                                                                                                                                                                                                                                                     New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerProvalileGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 531 BP; 158 A; 91 C; 130 G; 152 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 531
65
6
0
0
/note= "No start and stop codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                         Claim 10; SEQ ID NO 26; 135pp; English.
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                                                                                                                                                                                          Kim J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.59e-42
343.00
92.21%
84.42%
87.28%
                                                                                  02-JAN-2004; 2004US-00751235
                                                                                                        02-JAN-2004; 2004US-00751235
                                                                                                                                                                                            Dellapenna D, Tian L,
                                                                                                                                   (DELL/) DELLAPENNA D.
(TIAN/) TIAN L.
(KIMJ/) KIM J.
                                                                                                                                                                                                                       WPI; 2005-487984/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                 GENBANK; BE552887.
                                                                                                                                                                                                                                     P-PSDB; AEB16922
                             US2005150002-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CYP97C) CDNA.
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DB:
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180 9

Plant full length insert polynucleotide seqid 32608.

(first entry)

21-APR-2005

ADX61765

2 × 2 × 5 × 8

ΒP

ADX61765 standard; cDNA; 1804

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New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; heat tolerance; drought tolerance; heat tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
                                                                                                                                                                                                                                                                                                   Cao Y;
                                                                                                                                                                                                                                                                                                    Tabaska JE,
                                                                                                                                                                                                                                                                                                   Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 32608; 15pp; English.
                                                                                                                                                                                                                                                                                                   Zhou Y, Kovalic DK,
                                                                                                                                                                                          06-MAY-1999; 99US-00304517
05-NOV-2001; 2001US-00985678
                                                                                                                                                                      28-APR-2003; 2003US-00425114
                                                                                                                                                                                                                         LIU J.
ZHOU Y.
KOVALIC D K.
SCREEN S E.
                                                                                                                                                                                                                                                                                                                     WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                   TABASKA J E CAO Y.
                                                                                                                                                                                                                                                                                                                                                                         improving yield.
                                                                                                                            US2004034888-A1
                                                                                                         Unidentified
                                                                                                                                                  19-FEB-2004
                                                                                                                                                                                                                                                                  (TABA/)
(CAOY/)
                                                                                                                                                                                                                                              (KOVA/)
(SCRE/)
                                                                                                                                                                                                                          (1001/)
                                                                                                                                                                                                                                                                                                   Liu J,
                                                                                                                                                                                                                                     /nonz)
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The invention describes a recombinant DNA construct comprising a polymucleotide consisting of a sequence encoding an amino acid sequence evaluable in electronic form from the US patent office at the available in electronic form from the US patent office at the polymucleotide of the sequence. The following the polymucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, ignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one extra content. This sequence represents a plant full length insert content. This sequence represents a plant full length insert the can be used in the recombinant DNA construct of the invention.

Sequence 1804 BP; 464 A; 392 C; 472 G; 476 T; 0 U; 0 Other;

Alignment Scores:

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494 CTTGAGCCATATGCTTTGAGTGGGGAACCTGTCAATATGGAAGCGAGGTTTTCTCAGTTG 553
                                                                                                               1 LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet 20
1804
65
6
0
0
                         Conservative:
Mismatches:
 Length:
Matches:
                                                   Indels:
                                                                                        US-10-751-235-1 (1-77) x ADX61765 (1-1804)
 .44e-41
             343.00
92.21%
84.42%
87.28%
                                      Similarity:
                          Percent Similarity:
                                                 Query Match:
DB:
                                       Best Local
                                                                                                                                        요
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839

4.04e-41

Alignment Scores: Pred. No.:

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554 ACATTGGATGTGATTGTTATCATTGTTCAACTACAATTTTGATTCCCTCACAAGAT 613
                                                                          614 AGTCCTGTCATTGATGCTGTTTATACTGCACTCAAAGAAGCAGAGCTTCGTTCTACAGAT 673
40
                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to genes, proteins and methods comprising carctenoid monoxygenases in the cytochrome P450 family. The invention also relates to altering carctenoid ratios in plants and microorganisms using LUTI epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carctenoid production in a plant for enhancing production of specific carctenoid compounds that are potent antioxidants. The present sequence is tomato cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Tomato cytochrome P450 97C (CYP97C) protein"
                                                                                                                                                                                                                                                                                                                                    Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97C;
                                                         SerProvalileGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                                                     77
                                                                                                                     LeuLeuProTyrTrpLys1leAspAlaLeuCysLys1leValProArgGln
                                                                                                                                     CTTTTGCCATACTGGAAGGTTGGTTTCTTGTGCAAGATAATCCCAAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 839 BP; 251 A; 160 C; 190 G; 238 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                     Tomato cytochrome P450 97C (CYP97C) cDNA, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "No start and stop codons"
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                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim J;
                                                                                                                                                                                                                                                                                                                                                   cytochrome P450 97C; gene; ss.
                                                                                                                                                                                                             AEB16927 standard; cDNA; 839
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                                                                                                                                                                                                                                                                        (first entry)
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TIAN L.
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                                                                                                                                                                                                                                                                        08-SEP-2005
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                                                                                                                                                                                                                                            AEB16927;
71
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(TIAN/)
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08-SEP-2005
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/*tag= a
product= "Wheat cytochrome P450 97C (CYP97C) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                               LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
                                                                                                         ThrLeukspVallleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
                                                                                                                                           SerProValIleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
                                                                                                                                                                             Wheat cytochrome P450 97C (CYP97C) cDNA, SEQ ID NO: 24.
00020
        Conservative:
Mismatches:
Indels:
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  Matches:
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                                     Gaps:
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/note= "No stop codon"
                                                     x AEB16927 (1-839)
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337.00
92.21%
85.71%
85.75%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DELL/) DELLAPENNA (TIAN/) TIAN L. (KIMJ/) KIM J.
                                                                                                                                                                                                                                                                                                                                     Triticum aestivum.
         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                      US-10-751-235-1 (1-77)
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The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention

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also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is wheat cytochrome P450 monooxygenase
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/*tag= a /*tag= a /*tag= barley cytochrome P450 97C (CYP97C) protein" /*product= "Barley cytochrome P450 97C (CYP97C) protein" //transl except= (pos:1585. .1587, aa:Kaa) //transl except= (pos:1585. .1587, aa:Kaa) //transl except= "Xaa may be any naturally occurring amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           engineering; antioxidant; transgenic plant; CYP97C;
                                                                                                                                                                                                                                                                                                                                                ThrLeuAspValileGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                         SerProvalileGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
                                                                                                                                                                                                                                                                                       LeuGlnProTyralaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuleuProTyrTrpLyslleAspAlaLeuCysLyslleValProArgGln 77
                                                                                                       BP; 243 A; 298 C; 295 G; 250 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barley cytochrome P450 97C (CYP97C) cDNA, SEQ ID NO: 23
                                                                                                                                                    1086
65
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Matches:
Conservative:
Mismatches:
Indels:
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Hordeum vulgare; subsp. spontaneum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JAN-2004; 2004US-00751235
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335.00
90.91%
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85.24%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pigment, metabolic
                                                                                                                                                                                                     Best Local Similarity:
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                                                                                                                                                                                       Percent Similarity:
                                                                                                               Sequence 1086
                                                                                   (CYP97C) CDNA
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Kim J;

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02-JAN-2004; 2004US-00751235.
                                                                           Dellapenna D, Tian
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                              (DELL/) DELLAPENNA
(TIAN/) TIAN L.
(KIMJ/) KIM J.
                                                                                                         P-PSDB; AEB16918.
DDBJ; AK065689.
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DB:
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                                                                                                                 The present invention relates to genes, proteins and methods comprising carotenoid monoxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is barley cytochrome P450 monooxygenase (CYP97C) cDNA.
                                                                                                                                                                                                                                                                                                                                                              634 ACACTAGATGTGATTGGTTTGTTTGTTCAACTACAACTTTGATTCCCTCACATTCGAT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                  694 AGTCCTGTTATTGATGCTGTTTACACCGCACTGAAAGAAGCAGGGGGGCTCGTTCTACAGAT 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Rice cytochrome P450 97C2 (CYP97C2) protein"
                                new expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotemoid production in a plant for enhancing production of specific carotemoid compounds.
                                                                                                                                                                                                                                                                                                                                                                                           ThrLeuAspVallleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
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                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                  Sequence 1638 BP; 406 A; 403 C; 427 G; 401 T; 0
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                                                                                              Claim 10; SEQ ID NO 23; 135pp; English.
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P-PSDB; AEB16919.
GENBANK; BM816653, BU987393, CA023004
DDBJ; AV835803.
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335.00
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Query Match:
DB:
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                                                                                                                                                                   The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidates. The present sequence is rice cytochrome P450 monooxygenase
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New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
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Matches:
Conservative:
Mismatches:
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                                                                                                                        Claim 10; SEQ ID NO 22; 135pp; English
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335.00
90.91%
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                                                                                                                                                                                                                                                                                                                                                 (CYP97C2) cDNA.
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CDS

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160 GGTCTGGACATCATCGGCAAGGCCGTGTTCAACTACGACTTCGACTCGCTGGCGCACGACGAC 219
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                                                                                                                                                                                                                                   "Green algae cytochrome P450 97A (CYP97A) like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
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                                                                                           Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97A; cytochrome P450 97A; gene; 88.
                                                           Green algae cytochrome P450 97A (CYP97A) like cDNA, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1101 BP; 217 A; 353 C; 342 G; 189 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                       /note= "No start and stop codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
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                                                                                                                                                                                     Location/Qualifiers
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210.00
72.73%
53.25%
53.44%
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                                                                                                                                                                                                                       /*tag= a
/product=
                                  (first entry)
                                                                                                                                                    Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                           protein"
                                                                                                                                                                                                                                                                             partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dellapenna D, Tian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-487984/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DELL/) DELLAPENNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                             US2005150002-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TIAN/) TIAN L.
(KIMJ/) KIM J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                  08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                               07-JUL-2005
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AEB16950;
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                                                                                                                                                                                          Key
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LuTl epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is sunflower cytochrome P450 monooxygenase (CYP97C) CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                 New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuGlnProTyralaGluAspGlySeralaValAsnMetGluAlaLysPheSerGlnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTAAGATCATACGCACGCAGTGACACGTCTTAACATGGAGCAACAGTTTTCGCAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrLeuAspVallleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerProvalileGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTGCCATATTGGAAGATAAGTGCGTTATGTAAGATTATACCAAGACAA 483
                                   "Sunflower cytochrome P450 97C (CYP97C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuleuProTyrTrpLys1leAspAlaLeuCysLys1leValProArgGln 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 186 A; 110 C; 144 G; 184 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      008000
                                                                                       stop codons"
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Mismatches:
Indels:
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Matches:
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                                                                                         and
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                                                                                         /note= "No start
                                                                                                                                                                                                                                                                                                                                    Kim J;
                                                                                                                                                                                              02-JAN-2004; 2004US-00751235
                                                                                                                                                                                                                                02-JAN-2004; 2004US-00751235
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319.00
89.61%
77.92%
81.17%
                     /*tag= a
/product=
                                                         protein"
                                                                           'partial
       1. .624
                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                              (DELL/) DELLAPENNA D.
(TIAN/) TIAN L.
(KIMJ/) KIM J.
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-487984/49.
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                                                                                                                             US2005150002-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 624
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Query Match:

Pred. No.:

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RESULT 12 AEB16950 20

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AEB16948;

RESULT 13 AEB16948

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484 AATGGAATAGTTGAGGCTGTGTATGTAACATTACGGGAAGCGGAAAATGCGGAGCACATCT 543
                                                                                                                                                                                                                                                                         41 SerProVallleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag= a
product= "Barley cytochrome P450 97A (CYP97A) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97A; cytochrome P450 97A; gene; 88.
                                                                                                                     1 LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
                                                                                                                                                                                                                       424 ACGCTGGATGTCATCGGGAAGGCAGTGTTCAATTATGATTTTGATTCATTATCATTACGAT
                                                                                                                                                                                               ThrLeuAspValIleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
                                                                                                                                                                                                                                                                                                                                                                             544 CCTATTCCAACTTGGGAAATACCCATATGGAAAGACATCTCCCCTCGGCAG 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDBJ; BJ480615, BJ485000, BJ448041, BJ455787, AV910152, AV938407.
EMBL; AJ477620, AJ477618, AJ477619, AJ832622.
                                                                                                                                                                                                                                                                                                                                                   LeuLeuProTyrTrpLyslleAspAlaLeuCysLyslleValProArgGln 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barley cytochrome P450 97A (CYP97A) cDNA, SEQ ID NO: 44.
     Mismatches:
Indels:
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GENBANK; CA004011.
                                           Gaps:
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                                                                                 US-10-751-235-1 (1-77) x ABB16948 (1-1031)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare; subsp. vulgare.
Hordeum vulgare; subsp. spontaneum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEB16946 standard; cDNA; 1527 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim J;
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     53.25<del>8</del>
52.678
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TIAN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-487984/49.
Best Local Similarity:
Query Match:
DB:
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(TIAN/) 7
(KIMJ/) P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 GACCCGGTCATCCAGGCGGTGTACATGCTGCGCGAAGCGGAAGCGGACGCTCCACAGCG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is wheat cytochrome P450 monooxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Wheat cytochrome P450 97A (CYP97A) protein"
frams1 except= (pos:592. .595, aa:Gln)
partia1
'note= "No start codon"
                                                                                                                                                                                                                                                                                                                               engineering; antioxidant; transgenic plant; CYP97A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                     280 CCCATGGCCTACTGGAACATTCCCGGCATCCAGTTTGTGGTGCCGCGGGAG 330
                                                           61 LeuLeuProTyrTrpLyslleAspAlaLeuCysLysIleValProArgGln 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1031 BP; 253 A; 237 C; 284 G; 257 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                         Wheat cytochrome P450 97A (CYP97A) cDNA, SEQ ID NO: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1031
41
14
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Matches:
Conservative:
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1. .1031
                                                                                                                                                                             BP
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                                                                                                                                                                         AEB16948 standard; cDNA; 1031
                                                                                                                                                                                                                                                                                                                           Pigment; metabolic engineering cytochrome P450 97A; gene; ss
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207.00
71.43%
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DDBJ; BJ238659, BJ233019.
GENBANK; CD882035.
                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DELL/) DELLAPENNA
(TIAN/) TIAN L.
(KIMJ/) KIM J.
                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .PSDB; AEB16939.
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Percent Similarity:

Pred. No.:

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480
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                                                                                                                                                                                                                                                                                                                                                   SerProVallleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp 60
                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97A; cytochrome P450 97A; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .1899
/*tag= a
/product= "Rice cytochrome P450 97A (CYP97A) protein"
                                                                                                                                                                                                                                                        LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
                                                                                                                                                                                                                                                                                                      ThrieuAspValileGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrAsp
                                                                                                                                                                                                                                                                                                                    591
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                                                                                                                                                                                                                                                                                                                                                                                                    LeuLeuProTyrTrpLy81leAspAlaLeuCy8Ly81leValProArgGln
                                                                                                                                                                                                                                                                                                                                                                                                                    541 CCTATTCCAACATGGGAAATACCCATATGGAAAGACATCTCCCCTCGGCAG
                                                                                                           Sequence 1527 BP; 399 A; 343 C; 395 G; 390 T; 0 U; 0 Other;
                                                                                                                                               1527
41
14
22
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytochrome P450 97A (CYP97A) DNA, SEQ ID NO: 43
                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                    x AEB16946 (1-1527)
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207.00
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P-PSDB; AEB16936.
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(TIAN/) TIAN L.
(KIMJ/) KIM J.
                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                     US-10-751-235-1 (1-77)
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                                                                                                                                                                            Percent Similarity
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                                                                                                                                         Alignment Scores:
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DB:
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The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is rice cytochrome P450 monooxygenase (CYP97A) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 SerProVallleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrLeuAspVallleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
                  New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LeuLeuProTyrTrpLysileAspAlaLeuCysLysileValProArgGln
                                                                                                                                                                                                                                                          Sequence 1899 BP; 454 A; 470 C; 504 G; 471 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                Claim 10; SEQ ID NO 43; 135pp; English
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206.00
71.43%
53.25%
52.42%
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Query Match:
DB:
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DDBJ; AP004028
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43, Appl 43, Appl 43, Appli 6, Appli 5, Appli 5, Appli 3, Appli 1, Appli 1, Appli

Perfect score:

Run on:

Sequence:

Scoring table:

Minimum DB Maximum DB

Searched:

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APPLICANT: Siminazky, Balaza
APPLICANT: Siminazky, Ralph B.
APPLICANT: Dewey, Ralph B.
APPLICANT: Dewey, Ralph B.
APPLICANT: Corbin, Fracerick T.
TITLE OF INVENTION: No. 6121512e1 Cytochrome P-450 Constructs and
TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEB: Virginia C. Bennett
STREET: PO BOX 37428
CITY: Raleigh
STATE: No. 6121512th Carolina
COUWRRY: USA
ZIP: 27627
                       Sequence 6, Appli
Sequence 4077, Ap
Sequence 92, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 21, Appli
                                                                                                                                                                                                                                                                                  Sequence 43, Appl
Sequence 43, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 14033, A
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Sequence 2487, Ap
Sequence 1060, Ap
Sequence 121, App
Sequence 3332, Ap
Sequence 3132, Ap
Sequence 4116, Ap
                                                                                                                                                                                                                            Sequence 11,-App
Sequence 12358,
                                                                                                                                                                                                                                                                      Sequence 43,
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATR:
APPLICATION NUMBER: US/08/948,564
US-08-802-141-3

US-08-911-321-6

US-09-248-796A-4077

US-09-712-363-92

US-09-133-192

US-09-073-594-2

US-09-073-594-2

US-09-073-594-2

US-09-103-840A-1

US-09-336-115C-21

US-09-336-115C-21

US-09-336-115C-21

US-09-336-115C-21

US-09-336-115C-21

US-09-336-115C-21

US-09-349-016-1235

US-09-268-992-6

US-09-268-992-6

US-09-268-992-3

US-09-269-916-12777

US-09-949-016-12777

US-09-949-016-1220

US-09-949-016-1220

US-09-949-016-1220
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CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REPERNICE/DOCKET NUMBER: 5051-409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 15, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
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1431
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US-08-948-564-15
                                                                                                                                                                                                             Command :line parameters:
-MODEL=frame+ p2n.model - 12012x1bh
-Q=/cgn2_1/USPTO-51235/runat 12012006_120916_2538/app_query.fasta_1.263
-Q=/cgn2_1/USPTO-spool/US10751235/runat 12012006_120916_2538/app_query.fasta_1.263
-Q=/cgn2_1/USPTO-spool/US10751235/runat 12012006_120916_2538/app_query.fasta_1.263
-USPTO-BEATSO - UNITS=bits -STRAT=1 - END=-1 - MATRIX=blosum62 - TRANS=buman40.cdi
-LIST=45 - DOCALIGN=200 - THR SCORES=pct - THR MAX=100 - THR MN=0 - ALIGN=15
-USRE-US10751235 @CGN 1 1 193 @runat 12012006_120916_2538 - NCPU=6 - ICPU=3
-NO MAAP - LARGEQUERY - NEG SCORES=0 - WALT - DSPBLOCK=100 - LONGIAG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THRADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DBLOP=6 - DBLEXT=7
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Sequence 7, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 11, Appli
                                                                                                                                      January 15, 2006, 12:59:30 ; Search time 171 Seconds (without alignments) 800.423 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                               1 LQPYAEDGSAVNMEAKFSQM.....STDLLPYWKIDALCKIVPRQ
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'Cgm2 6/prodata11/ina/1 COMB.seq:*

'Cgm2 6/prodata11/ina/5 COMB.seq:*

'Cgm2 6/prodata11/ina/6A COMB.seq:*

'Cgm2 6/prodata11/ina/6B COMB.seq:*

'Cgm2 6/prodata11/ina/R COMB.seq:*

'Cgm2 6/prodata11/ina/H COMB.seq:*

'Cgm2 6/prodata11/ina/P COMB.seq:*

'Cgm2 6/prodata11/ina/PP COMB.seq:*

'Cgm2 6/prodata11/ina/PP COMB.seq:*

'Cgm2 6/prodata11/ina/PP COMB.seq:*

'Cgm2 6/prodata11/ina/RB COMB.seq:*

'Cgm2 6/prodata11/ina/RB COMB.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                    OM protein - nucleic search, using frame_plus_p2n model
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US-09-615-192A-156
US-09-169-189-156
US-10-018-730A-3
US-09-583-447A-7
US-09-583-447A-3
US-09-583-447A-1
US-09-583-447A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                               1303057 seqs, 888780828 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                     BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Rgapop 6.0, Pgapext
Delop 6.0, Delext
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seq length: 200000000
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Database

200 196 196 76 71.5 71.5 71.5

Result No.

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US-10-751-235-1 (1-77) x US-09-615-192A-156 (1-404)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Blokeberg, Leonard N.
APPLICANT: Havukkala, 11kka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.26e-20
196.00
74.63%
58.21%
    TELEFAX: 919-854-1401
INFORMATION FOR SEC ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 1831 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                      2.57e-20
200.00
73.24%
56.34%
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                                                                                                                         NAME/KEY: CDS
LOCATION: 20..1747
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Best Local Similarity: {
Query Match:
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US-09-615-192A-156
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Pred. No.:
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31 AsnīyrAsnPheAspSerLeuThrThrAspSerProVallleGluAlaValTyrThrAla 50
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                                                                                                                                                                                                                                                                                            Sequence 156, Application US/09169789
; Sequence 156, Application US/09169789
; Patent No. 6653528
; GENERAL INFORMATION:
; APPLICANT: Bloksbarg, Leonard N.
; APPLICANT: Bloksbarg, Leonard N.
; TITLE OF INVENTION: Modification of Plant Lignin Content; TILE REFERENCE: 11000.1003c2
; CURRENT APPLICATION NUMBER: US/09/169,789
; CURRENT APPLICATION NUMBER: US 08/975,316
; EARLIER PILING DATE: 1998-10-09
; EARLIER PILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: US 08/713,000
; RARLIER PILING DATE: 1996-09-11
; NUMBER: OF SEQ ID NOS: 185
; SOFTWARE: FREED for Windows Version 3.0
; SEQ ID NO 156
; LENGTH: 404
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Matches:
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                                                                                                                                                                                                     71 CysLysileValProArgGin 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.26e-20
196.00
74.63%
58.21%
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ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-169-789-156
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US-10-018-730A-3
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GENERAL INCORNATION:
APPLICANT: WOJNOWSKI, Leszek
APPLICANT: WOJNOWSKI,
Klaus
APPLICANT: BISELY, Regina
APPLICANT: GELAGE,
REGINA
TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
TITLE OF INVENTION: (CYP3A) GENE PAMILY: CYP3AX
FILE REPERENCE: 310115.401
CURRENT PILITED DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09583447A

Sequence 10. 645745

Patent No. 645745

APPLICANT: BELLNER, Klaus

APPLICANT: GELLNER, Klaus

TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
                            479 CTGAGGCAGGAAGCAGAAAAAGCAGCAAGATCCATCAAAAAGATTTCTTTGGGGCCTAC 537
                                                                                                   |||:::|||||||||
538 ACCATGGATGTAATCACTGGCACATTATTTGGAGTGAACTTGGATTCTCTCAACAATCCA 597
                                                                           21 ThrLeuAspValileGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThr--- 39
                                                                                                                                                  40 AspSerProVallleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThr 59
         LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 ThrLeuAspVallleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThr -- 39
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                                                                                                                                                                                                                                                            655 TTTTTACTCTTAATATACAGAGTCTCGCTGTGTTGC 690
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Matches:
Conservative:
Mismatches:
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Gaps:
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71.50
54.72%
33.96%
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FEATURE:
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Best Local Similarity:
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LENGTH: 1349
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US-09-583-447A-5
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APPLICANT: WOLNOWSKI, Leszek
APPLICANT: WOLNOWSKI, Leszek
APPLICANT: GELLIER, Klaus
APPLICANT: EISELT, Regina
TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
TITLE OF INVENTION: CYP3A) GENE FAMILY: CYP3AX
FILE REPERENCE: 310115,401
CURRENT APPLICATION NUMBER: US/09/583,447A
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATCHIIN Ver. 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnTyrAsnPheAspSerLeuThrThrAspSer-----ProValIleGluAlaValTyr 48
APPLICANT: Jonathan, Jones
TITLE OF INVENTION: PROCESS FOR OXIDISING AROMATIC COMPOUNDS
FILE REPERENCE: P02353US1 / 10112404 / N.76277B
CURRENT APPLICATION NUMBER: US/10/018,730A
CURRENT FILING DATE: 2002-04-04
FRIOR PRILING DATE: 1002-04-04
FRIOR PRILING DATE: 2000-06-18
FRIOR APPLICATION NUMBER: PCT/GB00/02379
FRIOR APPLICATION NUMBER: PCT/GB00/02379
FRIOR APPLICATION NUMBER: PCT/GB00/02379
FRIOR PRILING DATE: 2000-06-18
FRIOR PRILING DATE: 2000-06-18
SROFWARE: PAECHTIN Version 3.1
SEQ ID NO 3
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Indels:
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Matches:
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                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                   0.432
76.00
56.52%
39.13%
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29.17%
18.83%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-583-447A-7
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Pred. No.:
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US-09-583-447A-7
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; Sequence 1, Application US/09583447A
; Patent No. 6645745
; GENERAL INFORMATION:
    APPLICANT: WOLNOWSKI, Leszek
; APPLICANT: GELLMER, Klaus
; APPLICANT: GELLMER, Klaus
; TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
; TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
; FILE REFERENCE: 310115.401
; CURRENT APPLICATION NUMBER: US/09/583,447A
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1659
; TYPE: DNA
; TYPE: DNA
; PERATURE PATENTE CONDITION OF A NEW MEMBER OF SEQ ID NO 1
; SEQ ID NO 1
; REQUENT OF THE CONDITION OF SEQ ID NO SEQ ID
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Matches:
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FILE REFERENCE: 310115.401
CURRENT APPLICATION NUMBER: US/09/583,447A
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 1515
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                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (1)..(1515)
US-09-583-447A-3
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LOCATION: (109
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Pred. No.:
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US-09-583-447A-1
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Sequence 11, Application US/09583447A

Sequence 11, Application US/09583447A

Patent No. 6645745

GENERAL INFORMATION:

APPLICANT: WOJNOWSKI, Leszek

APPLICANT: WOJNOWSKI, Leszek

APPLICANT: BISELT, Regina

TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A

TITLE OF INVENTION: (CYPANA)

FILE REFERENCE: 310115.401

CURRENT PILING DATE: 2000-05-30

NUMBER: OF SEQ ID NOS: 45

SOFTWARE: PATENTIN Ver. 2.1

SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1000 ACCATGGATGTAATTGGAGTGAACTTGGATTGATTCTTCTCTCAAAATCCA 1059
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                     ThrLeuAspValileGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThr--- 39
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US-08-802-141-3
US-08-802-141-3
; Sequence 3, Application US/08802141
; Patent No. 5773009
; GENERAL INFORMATION:
APPLICANT: GELASS, ROGER I.
APPLICANT: GENTSCH, JOHN R.
APPLICANT: BHAN, M. K.
TITLE OF INVENTION: ROTAVIRUS STRAIN AND RELATED
TITLE OF INVENTION: COMPOSITIONS
; TITLE OF INVENTION: COMPOSITIONS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
ADDRESSE: NEEDLE & ROSENBERG, P.C.
STREET: LITP PEACHTEE STREET; Suite 1200
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                                                                             40 AspSerProValIleGluAlaValTyrThrAlaLeuLys
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Mismatches:
Indels:
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OTHER INFORMATION: n=a, c, t or
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54.72%
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Query Match:
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; Sequence 4077, Application US/09248796A
; Patent No. 6747137
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CELL TYPE: N/A
Michigan
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Best Local Similarity:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 IleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAspLeuLeuPro 63
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             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOUTAME: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,141
FILING DATE: 19-FEB-1997
CLASSIPICATION NUMBER: 08/231,041
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sprakt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.609
TELECOMMUNICATION NUMBER: 1414.609
TELECOMMUNICATION NUMBER: 1250.016
REFERENCE AD4.6688-0770
TELEFAX: 688-9880
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 2352 base pairs
SEQUENCE CHARACTERISTICS:
LENGTH: 2352 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: Inneat
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence (Application US/08911321)
Patent NO. 6010703
GENERAL INFORMATION:
FITLE OF INVENTION: Recombinant Poxvirus
TITLE OF INVENTION: Peline Rhinotracheitis
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: 1an C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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71.00
46.77%
33.87%
18.07%
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Best Local Similarity:
Query Match:
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; LOCATION:
US-08-802-141-3
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3728 GCTGATGTATTTGGCCTTTCGGTGTTTTGTTTTACTCGTTCGATACGCGTGGTCATCGACAT 3787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMetThr-
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Matches:
Conservative:
Mismatches:
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IDENTIFICATION METHOD: Sequencing
OTHER INFORMATION: DNA encoding PK, gG, gD,
OTHER INFORMATION: g1, gB
ZIP: 48864
COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-751-235-1 (1-77) x US-08-911-321-6 (1-6176)
                                                          MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS.DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,321
FILING DATE:
CLASSIPICATION BYTA:
APPLICATION NUMBER: US/08/911,321
APPLICATION NUMBER: US/08/9183
FILING DATE: July 26, 1933
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. MCLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-1!
TELECHONE: (517) 347-4100
TELEFRAX: (517) 347-4103
TELEX: No. 60107034
INFORMATION FOR SEQ ID NO: 6:
LENGTH: 6176
TELEGTH CALLOR OF SEG ID NO: 6:
LENGTH: 6176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Nucleic Acid
STRANDEDNES: Double
TOPOLOGY: Linear
MOLECULE TYPE:
DESCRIPTION: DNA
HYPOTHETICAL: No
ANTI-SENSE: No
ORIGINAL SOURCE:
ORGANISM: Feline herpesvirus-1
STRAIN: 1
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45.61
33.33
18.07
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301 GACGATGGCGCAGCGTTG----- 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 AlayalTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAspLeuLeuPro-TyrTr 65
                                                                                                                                                                                                                                                                                                                                                                                                         6 GluaspGlySerAlaValAsnMetGluAlaLysPheSerGlnMetThrLeuAspVallle 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 GlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAspSerProVallleGlu 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/07603133B
| Sequence 19, Application US/07603133B
| Patent No. 5298244
| GENERAL INFORMATION:
| APPLICANT: Redemond, Mark J.
| APPLICANT: Parker, Michael D.
| TITES OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE NUMBER OF SEQUENCES: 30
| CORRESPONDENCE ADDRESS: ADDRESSEE: MORTISON & FOETSET: STREET: 545 Middlefield Road, Suite 200
| CITY: Menlo Park
                                                                                                                                                                                                                           2217
21
12
12
25
11
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RODIES ROBERT 33,208
REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 9313-0004.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 327-2251
                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                     US-10-751-235-1 (1-77) x US-09-712-363-92 (1-2217)
                                                                                                                                                                                                                                                                                                              Indels:
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SEQ TWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 92
LENGTH: 2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 Greerceeecrccecrececarc 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pLysileAspAlaLeuCysLysile 73
                                                                                                                            ; TYPE: DNA; ORGANISM: Mycobacterium tuberculosis US-09-712-363-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 706141
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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47.83$
30.43$
17.56$
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COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
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        GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR PELLING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
RIOR FILING DATE: 1998-02-13
RIOR FILING DATE: 1998-02-13
RUMBER OF SEQ ID NOS: 28208
SEQ ID NO 4077
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 92. Application US/09712363
| Sequence 92. Application US/09712363
| Sequence 92. Application US/09712363
| Patent No. 6892139
| GENERAL INFORMATION:
| APPLICANT: Eisenberg, David
| APPLICANT: Rottein, Sergio H.
| APPLICANT: Marcotte, Edward M.
| TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
| TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
| TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
| CURRENT APPLICATION NUMBER: US/09/712,363
| CURRENT FILING DATE: 2000-01-13
| PRIOR FILING DATE: 2000-02-01
| PRIOR FILING DATE: 2000-02-01
| PRIOR FILING DATE: 1999-02-01
| PRIOR FILING DATE: 1999-03-26
| PRIOR FILING DATE: 1999-03-26
| PRIOR FILING DATE: 1999-05-14,093
| PRIOR FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 AAAAAGGCTCAAATAAGTTCAGAGATATTGCCCAAAATCAAAATAGACTTGCCGTGT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 TyrAsnPheAspSerLeuThrThrAspSerProValIleGluAlaValTyrThrAlaLeu 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlualaLysPheSerGlnMetThrLeuAspValIleGlyLeuSerLeuPheAsn----- 31
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118
24
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                              0.261
69.50
53.97%
28.57%
17.68%
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US-09-248-796A-4077
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223 ACCATTTTA 231
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Best Local Similarity:
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US-09-712-363-92
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Search completed: January 15, 2006, 15:14:55
Job time : 177 secs
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                                                                                                                                                                                                                                                                                                                                                            4 TyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMetThrLeuAsp 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 IleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAspLeuLeuPro 63
                                                                                                                                                                                                                                                                                                                                                                                                                                    24 ValileGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAspSerProVal 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-653-740-2
; Sequence 2, Application US/08653740
; Sequence 2, Application US/08653740
; Patent No. 5792850
; GENERAL INFORMATION:
APPLICANT: James W. Baumgartner
APPLICANT: Brank J. Grant
; APPLICANT: Rrank J. Grant
; TITLE OF INVENTION: HEMATOPOIETIC CYTOKINE RECEPTOR
; WUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
ADDRESSE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
ZIP: "."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/653,740
FILING DATE:
CLASSIFICATION: 4335
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31,648
REGISTRATION NUMBER: 95-31
TELECOMMUNICATION: INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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| LENGTH: 2363 base pairs | TYPR: NUCLEIC ACID | TYPR: NUCLEIC ACID | STRANDEDNESS: double | TOPOLOGY: linear | MOLECULE TYPE: CDNA | FRAUTRE: | NAME/KEY: CDS | LOCATION: 10..2337 US-07-603-1338-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: 206-442-6678
INPORMATION POR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 2368 base pairs
                                                                                                                                                                                               3.37
69.00
45.16%
33.87%
17.56%
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                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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2060 CCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGCAGGCCAAGGTGGAAGGATCACTTAG 2119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::
2000 AGAGTGGCAGCTGCCTAAATCTGTTCCGCTGTAACAGAACTGAATTTGGACCCCAG 2059
                                                                                                                                                                                                                                                                                                                                                                  1 LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet 20
                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ThrLeuAspVallleGlyLeuSerLeuPheAsnTyrAsn------Phe-AspSerLe 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 uThrThrAspSerProValIleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 gSerThrAspleuLeuProTyrTrpLysIleAspAlaLeuCysLys 72
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24
12
33
7
                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                        3.38
69.00
47.37
31.58
17.56
; TYPE: nucleic acid
; STRANDENNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; PRATURE:
; NAME, KEY: CDS
; LOCATION: 23..1759
US-08-653-740-2
                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                          Alignment Scores:
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Perfect score:

Sequence:

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OM protein

Run on:

Scoring table:

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AJ486563 AJ486563
CA742365 w£11c.pk0
AJ43231 AJ43231
BU987393 HF14K04r
BH584135 BOHAD9OTP
CB255014 54-801836
DR952390 BST111553
CX541939 813ANF0BH
BI263819 NF114G06P
BH931006 odi10g10.
BH931006 odi10g10.
CZ719138 QHB9C20.
CZ710414 OC_Ba003
CZ799589 OC_Ba017
BQ862275 QGCZ0K13.
AJ615653 AJ615653
BZ822133 PUFGG89TD
CG618386 OGVAP09TH
CG056732 PUFTX10TB
CG056734 PUFTX10TB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unsuabyu 1664 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length CDNA Complete sequence from clone
GSLTFB26ZE04 of Flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CV538441 POD 005 F
BM003139 1031108G0
BJ480615 BJ480615
BJ234910 BJ234910
CX022870 MJ1v4-404
AV931345 AV939356
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 131 91006 EVRX cedex - FRANCE (B-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CW000851 ZMMBHg000
CZ321241 ZMMBF0023
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CL426941 ZMMBBD044
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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CD053804 HO03G16S
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TCf, GSLT. CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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CZ719589
BQ86275
AJ615653
BZ822133
CC618386
CG056732
CG394464
CG056734
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CZ321241
CV53841
BM003139
BJ480615
BJ234910
AV941342
AV933356
CG429086
    AJ486563
AJ42365
AJ433365
AJ433398
AJ5804
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2 (bases 1 to 1664)
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                                          VERSION
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DEFINITION
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AUTHORS
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AUTHORS
TITLE
JOURNAL
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CNSOASYJ
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10751235/runat_12012006_120915_2527/app_guery.fasta_1.263
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-DB=SST_-QFWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-USRR-USI0751235_GCGN 1 1 5315_GTUNTAT -12012006_120915_2527 -NCPU=6 -ICPU=3
-NO NWAAP -LAAGBGUERY -MEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGIAG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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BX827285 Arabidops
CO072553 GR Ea31M
CW839414 GT8284.DB
BES22887 946086H10
CX290930 EST753644
BG643819 EST523044
                                                                                                                                       ; Search time 3032 Seconds
(without alignments)
1188.194 Million cell updates/sec
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                                                                                                                                                                                                                                                               LQPYAEDGSAVNMEAKFSQM.....STDLLPYWKIDALCKIVPRQ
                       GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                   nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                41078325 seqs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           January 15, 2006, 06:11:50
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CNS0A665
C0072553
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, Ygapext
, Fgapext
, Delext
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Maximum DB seq length: 200000000
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9b_est2:*
9b_htc:*
9b_est4:*
9b_est4:*
9b_est6:*
9b_est7:*
9b_9ss2:*
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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Database :

Score

Result Š 393 393 346 341 341

400450c

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Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage:
BP 191 91006 ENVR cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weatssenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
Length
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RATE TS-JUN-2004
GR EA31M14.r GR Ea Gossypium raimondii cDNA clone GR Ea31M14 3',
mRNA sequence.
CO072553
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Kim, H., Yu,Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C., Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                673 ACACTTGATGTCATTGGGTTGTCTCTTTTTAACTACAATTTCGATTCTTTGACTACTGAT 732
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Location/Qualifiers
1. 1709
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/db_xref="taxon:3702"
/clone="GSLTFB64ZA07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 ThrLeuAspValIleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
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Mismatches:
Indels:
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/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="At3g53130"
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Best Local Similarity:
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            TITLE
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CO072553
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids; eurosids II, Brassicales, Brassicaceae, Arabidopsis.

I (bases I to 1709)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Craud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Pull-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
      Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
UKGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length,
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB64ZA07 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
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Location/Qualifiers
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1. .1664
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                      /organism="Gossypium raimondii"
/mol_type="mRNA"
/mol_type="mRNA"
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/do="GR Ea3M14"
/tissue_type="whole seedlings"
/do=stage="fixst true leaves"
/do=lib="fixst true leaves"
/lab_host="fixst tru
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1 (bases 1 to 736)
May, B. P., Simorowski, J., Arroyo, J.-M., Vaughn, M.W., Shen, R., McCombie, W.R. and Martienssen, R.A.
Arabidopsis genomic sequences flanking Ds enhancer and gene traps in transgenic lines
Unpublished (2004)
Contact: Martienssen RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 CTGCAACCTTTTGCATTAGATGGCACTGCCGTGAACATGGAAGAAAAGTTTTCTCAACTG 155
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Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 1259
Fax: 520 621 1259
Email: rwing@gene.arizona.edu
Plate: 31 row: M column: 14.
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Conservative:
Mismatches:
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BE552887
946086H10.y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNa, mRNA sequence.
BE552887.1 GI:9794579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cold Spring Harbor Laboratory
1 Bungtown Rd., Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8322
Fax: 516 367 8369
Email: martiens@cshl.org
Transposon carrying a gene trap in line
GT8284. The transposon is located within At3g53130.
Class: transposon-tagged.
Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
/organism="Arabidopsis thaliana"
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/clone="GT8284"
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    (bases 1 to 531)
    Walbot, V.
    Maize ESTs from various cDNA libraries sequenced at Stanford

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Unpublished (1999)
Contact: Walbot V
Contact: Walbot V
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
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Matches:
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Indels:
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346.00
95.77%
95.77%
88.04%
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/tissue type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
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library, normalized, full-length"
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/note="vector: pCMVSport6.1; Site_2: NotI;
/notice="vector: pCMVSport6.1; Site_2: NotI;
/notIte="vector: pCMVSport6.1; Sit
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BST512013 tomato shoot/meristem Lycopersicon esculentum cDNA clone cT0732N21 5' sequence, mRNA sequence.
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

[ (bases 1 to 840)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerProvalileGluAlaValTyrThrAlaLeuLy8GluAlaGluLeuArgSerThrAsp 60
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Contact: CTGI
Clemson University Genomics Institute
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/ .
Seg primer: ATT TAG GTG ACA CTA TAG.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                            organism="Nicotiana benthamiana"
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/db_xref="taxon:4100"
/clone="NBMBY36"
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Nicotiana benthamiana
Nicotiana benthamiana
Nicotiana benthamiana
Nicotiana benthamiana
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Nicotiana.

E (bases 1 to 914)
S Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
L Unpublished (2003)
Other ESTS EST/53465
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               914 bp mRNA linear EST 02-AUG-2004 EST75364 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBMBY36 5'CK290930
                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: tassels; Vector: HybriZAP; Site_1: BCORI; Site_2: XhoI; George Chuck dissected immature tassels between Imm and 3mm. Sharon Stanfield prepared the CDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                   /db_xref="taxon:4577"
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inflorescence development"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     crigageccarariecrirreagresesaaccrercarararesaasceagerrircreagres 60
                                                                                                                                                                                                                                                                                                                                                    /clone_lib="946 - tassel primordium prepared by Schmidt
lab"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 SerProVallleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThreewaspValileGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
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Matches:
Conservative:
Mismatches:
Indels:
                     rel: 650 723 2227
Fax: 650 725 8221
Email: walbotostanford.edu
Plate: 946086 row: H column: 10.
Location/Qualifiers
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                                                                                                                                                                           /organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
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343.00
92.21%
84.42%
87.28%
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CK290930
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ORIGIN

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/clone="S0001100041C11F1"
/dev stage="Devvloping seed"
/clone lib==S00011"
/note="12,15,18 days after pollination"
                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:

    .534
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/lab_hoste="DH108"
                                                                                                                                                                                                                                                            US-10-751-235-1 (1-77) x AJ486563 (1-480)
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Crop Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA742365.1 GI:25558188
EST.
                                                                                                                           1.38e-37
335.00
90.91%
84.42%
85.24%
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CA742365
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Hordeum vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

E 1 (bases I to 480)
Saren, A.-M.; Tanskanen, J., Paulin, L. and Schulman, A.H.
Barley EST's
Barley EST's
Contact: Schulman AH
Institute of Biotechnology
University of Helsinki
P.O. Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
Finland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ486563 S00011 Hordeum vulgare CDNA clone S0001100041C11F1, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 ACACTIGATGITATIGGCCTIGCACICITCAAITACAAITITGAITCCCTIACTGAC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 AGTCCAGTTATTGATGCAGTTTACACTGCACTAAAAGAAGCAGAACTCCGTTCAACTGAT 211
                                                                                                                                                                              /tissue_type="shoot/meristem"
/dev stage="developing shoots from 4-6wks old plants"
/dab_host="SOLR"
/lab_host="SOLR"
/loote="Lomato shoot/meristem"
/note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2:
Xhol; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 ThrieuAspValileGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 CTTTTACCTGATGCAATTTCTGGCTCTGCAGTGAATATGGAGGGAAAGTTTTCTCAACTA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 SerProValileGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LeuleuProTyrTrpLysIleAspAlaLeuCysLysIleValProArgGln 77
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    1. .840
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/culfivar="TA496"
/db xref="texon:4081"
/clone="cTOF92N21"
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Matches:
Conservative:
Mismatches:
Indels:

    .480
    /organism="Hordeum vulgare"
/mol_type="mRNA"
    /db_xref="taxon:4513"

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EST.
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337.00
92.21%
85.71%
85.75%
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Best Local Similarity:
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AJ486563
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w. 142365 534 bp mRNA linear EST 26-NOV-2002 wfllc.pk001.il3 wfllc Triticum aestivum cDNA clone wfllc.pk001.il3 5. end, mRNA sequence.
                                                                                                                                                                                                                                                     276 ACACTAGATGGTTTGGTTTGTCTTTGAACTACAACTTTGATTCCCTCACATCAGAT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum (bread wheat)
Triticum aestivum
Triticum aestivum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 534)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat GDNA Sequence
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 AGTCCTGTTATTGATGCTGTTTACACCGCACTGAAAGAAGCAGGGCTCGTTCTACAGAT 395
                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                           41 SerProValIleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp 60
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/note="Vector: pBluescript SK+; Site 1: EcoRI; Site_2:
Khol; Wheat (Triticum aestivum, Hi Line) flag leaf"
                                                                                                                                                                                                                           1 LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Fax: 302-631-2607
Fax: M13.
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286 ACACTAGATGTGATTGTTTGTTCAACTACAACTTTGATTCCCTCACATCAGAT 345
                                             41 SerProValIleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooldeae; Triticeae; Hordeum.

1 (bases 1 to 596)

Saren,A.-M., Tanskanen,J., Paulin,L. and Schulman,A.H.

Barley EST's

Unpublished (2002)

Contact: Schulman AH

Institute of Biotechnology
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                                                                                                                                    142 ACATTAGATGTGATTGGTTTATCCTTGTTCAACTACAACTTGATTCCCTCACATCAGAT 201
                                                                                                                                                                                                                                                            202 AGICCIGITATIGAIGCIGITIACACIGCACTCAAAGAAGCIGAGGCICGGIICIACAGAI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
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                                                                                                                       LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
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P.O. Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
Finland.
                                                                                                                                                                                                                                                                                        LeuleuProTyrTrpLysIleAspAlaLeuCysLysIleValProArgGln 77
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/organiem="Hordeum vulgare"
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/clone="50001100019A01F1"
/day taxge="Developing seed"
/clone lib="$00011"
/note="12,15,18 days after pollination"
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Mismatches:
Indels:
Gaps:
                     Conservative:
Mismatches:
Indels:
           Matches:
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                                                                                           x CA742365 (1-534)
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85.24%
          335.00
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Query Match:
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Best Local Similarity:
Query Match:
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                                                                                              US-10-751-235-1 (1-77)
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/lab host="XLIO-Gold"
/lab host="XLIO-Gold"
/clone lib="HF"
/clone lib="HF"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of CDNA); Site_2: XhoI (3'-end of CDNA); developing caryopsis, I6-25 DAF(days after flowing) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, Sall, PBLI). NOTE: Also due to the cloning system used Blue/white selection for recombinate is not 100% reliable. Average insert size is 940 bp"
                                                                                                           600 bp mRNA linear EST 22-OCT-2002 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                         Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnolhyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 600)
Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
Balchuk, Y., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
Compublished (2002)
Contact: Stein Nils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="caryopsis"
/dev_stage="developing caryopsis, 16-25 DAF (days after
flowering)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular Markers Group, Department Genbank
Molecular Markers Group, Department Genbank
Constitution of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600
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Mismatches:
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Gaps:
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|db_xref="GABI:247336"
|db_xref="taxon:112509"
|clone="HF14K04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: stein@ipk-gatersleben.de
Insert Length: 600 Std Brror:
Plate: 14 row: K column: 4
Seq primer: Ml3rev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-751-235-1 (1-77) x BU987393 (1-600)
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/cultivar="Barke"
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335.00
90.91%
84.42%
85.24%
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E 1 (bases 1 to 657)
S Jakoby, M., Stracke, R., Soerensen, T.R. and Weisshaar, B.
Arabidopsis thaliana cDNA library enriched in transcription factors thomblished (2003)
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 04992215062851
Email: Weisshaa@mpiz-koeln.mpg.de
Insert Length: 657 Std Brror: 0.00
Plate: 7 row: L column: 14
Seq primer: T7R; CTAATACGACTATAGGGA.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              54-E018363-019-007-L14-T7R MPIZ-ADIS-019 Arabidopsis thaliana CDNA clone MPIZp768L147Q 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_trizer.org.
/tissue_trizer.org.
/dev stage="tissue culture"
/lab_hogt="E. coli DHSalpha mcr"
/lab_hogt="E. coli DHSalpha mcr"
/clone lib="MplZ-ADIS-019"
/note="Vector: pSPORT1; Site_1: NotI primer adapter;
state_2: Sall primer adapter: RNA from cellculture (Ar7) 5
days after inoculation treated with 0.002 mM cycloheximid
for 2 h in the dark. Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de. This
for further information."
                                                                                                                                                                                                   Arabidopsis thaliana
Rukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                               99
                                                         41 SerProValIleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
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Matches:
Conservative:
Mismatches:
Indels:

    .657
/organism="Arabidopsis thaliana"
/mol_type="maNA"
/cultivar="At7"

                                                                                                                             61 LeuLeuProTyrTrpLy8-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
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|db_xref="taxon:3702"
|clone="MPIZp768L1470"
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Best Local Similarity:
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BOHAD90TF BOHA Brassica oleracea genomic clone BOHAD90, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica i Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 570)
Ayele,M., Haas, B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
genication to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)
                                                                    296 AGTCCTGTTATTGATGCTGTTTACACCGCACTGAAAGAAGAAGAGCTCGTTCTACAGAT 355
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                                                                                                                                              SerProvalileGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
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/clone="BOHAD90"
/clone=1b=BOHA"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                         61 LeuLeuProTyrTrpLysIleAspAlaLeuCysLysIleValProArgGln 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 301-838-0208
Email: cdrown@igr.org
DNA is from a doubled haploid provided by Tom Osborn.
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
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/organism="Brassica oleracea"
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/strain="TO1000DH3"
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                                                                                                                                                                                                                                                                                                                                                                     survey sequence.
BH584135
BH584135.1 GI:17836592
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Contact: Chris Town
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329.50
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BH584135/c
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Email: hodges@lifesci.ucsb.edu
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Invitrogen."
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326.00
89.61%
81.82%
82.95%
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Best Local Similarity:
Query Match:
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// Ab _xref="taxon:338618"
// Ab _xref="mRNA"
// Ab host="bling Ti (Ti and TS phage resistance)"
// Isb host="bling Ti (Ti and TS phage resistance)"
// Isb host="bling Ti (Ti and TS phage resistance)"
// Ab host="bling Ti (Ti and TS phage resistance)"
// Ab host="bling Ti (Ti and TS phage resistance)"
// Ab host="bling Ti (Ti and TS phage resistance)"
// Ab host="bling Ti (Ti and TS phage resistance)"
// Ab host="bling Ti (Ti and TS phage resistance) Tr (Ti and TS phage resistance) Tr (Ti and TS phage resistance) Tr (Ti and TS phage respectively) (Ti E 29% by weight respectively), 2) Medium (7-20 mm) and large (at or near anchesis) flower buds (65 & 35% by weight respectively) and 3) Shoot spical meristerms. A formosa. These plants were glown from seed in sand and at approximately I month root tissue and leaf tissue and at approximately I month root tissue and leaf tissue each set of tissue and pooled in the following proportions:

1.5% from sets 1 & 2, 1% from sets 3 & 4. From the pooled total RNA, mRNA was extracted for mest collected for total RNA, mRNA was extracted and enriched by total RNA was extracted from encountered and enriched by total RNA was extracted from encountered and enriched by total RNA was extracted from encountered and enriched for full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR952300 668 bp mRNA linear EST 02-AUG-2005 EST1143839 Aquilegia cDNA library Aquilegia formosa x Aquilegia pubescens cDNA clone CO1S013, mRNA sequence.
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Aquilegia formosa x Aquilegia pubescens
Bukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, Ranunculales,
Ranunculaceae, Aquilegia, Pooli C Poressitz, T Kramer E
                                                                                                                                                                                                                                                                                           40
                                                                               20
                                                                                                              1 LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
                                                                                                                                                                                           ThrLeuAspValIleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hodges, S.A., Remaink, W., Buell, C.R., Borevitz, J., Kramer, E., Nordborg, M. and Tomkins, J. Generation of ESTS from Aquilegia Generation of ESTS from Aquilegia Conter ESTS: EST1143838 Conteact: Scott Hodges Department of Ecology, Evolution and Marine Biology University of California, Santa Barbara Santa Barbara CA 93106, USA Fex: 805 893 7824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .668
/organism="Aquilegia formosa x Aquilegia pubescens"
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Seq primer: M13 Reverse.
Location/Qualifiers
                                 US-10-751-235-1 (1-77) x CB255014 (1-657)
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VERSION
KEYWORDS
SOURCE
ORGANISM
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COMMENT
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/cissue_type="wixed shoot and floral apical meristems, fissue_type="mixed shoot and floral apical meristems, flower buds, leaves and roots"
/lab_host="DH10B T1 (T1 and T5 phage resistance)"
/clone lib="Aquilegia cDNA library"
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/notice="Vector: pGNV SPORT6.1; Site_1: NotI;
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/note="Vector: pGNV SPORT6.1; Site_1: pGNV SPORT6.1; Site_1: NotI;
/notice="Vector: pGNV SPORT6.1; Site_1: pGNV SPO
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Aquilegia formosa x Aquilegia pubescens
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Ranunculaceae; Aquilegia.
1 (bases I to 886)
1 (bases I to 886)
Nordborg, M. and Tomkins J.
Generation of Esrs from Aquilegia
Unpublished (2005)
Other_ESTS: EST115533
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SST115534 Aquilegia CDNA library Aquilegia formosa x Aquilegia pubescens cDNA clone COlMZ40, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Scott Hodges
Department of Ecology, Evolution and Marine Biology
University of California, Santa Barbara
Santa Barbara, CA 93106, USA
Tel: 805 893 7813
Pax: 805 893 4724
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         Length:
Matches:
Conservative:
Mismatches:
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us-10-751-235-1.p2n.rst

weight respectively) and 3) Shoot apical meristems. A fourth set of tissue was collected from plants of A. formosa. These plants were grown from seed in sand and approximately! I month root tissue and leaf tissue of various developmental stages were collected (84 & 16\* by weight respectively). Total RNA was extracted from each set of tissue and pooled in the following proportions: 1.5% from sets 1 & 2, 1% from sets 3 & 4. From the pooled total RNA, mRNA, mRNA was extracted and enriched for full-length messages and then normalized with proprietary methods by Invitrogen.

ORIGIN

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 6.12e-36 326.00 89.61% 81.82% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: No.:

US-10-751-235-1 (1-77) x DR923995 (1-886)

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SerProValileGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp 60 41

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Search completed: January 15, 2006, 15:11:57 Job time : 3038 secs

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15200, A 23, Appl 22, Appl 245, Appl 945, Appl 46, Appl 46, Appl 37324, Appl 73, Appl 78, Appl

59515, A 55, Appl 110390,

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Perfect score: Sequence:

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Scoring table:

Minimum DB Maximum DB

Searched:

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Sequence 773, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT PILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 773
                                                                                                                                                                                                                                                                     Sequence 156, App
Sequence 54, Appl
Sequence 54, Appl
Sequence 15203, A
Sequence 54, Appl
Sequence 67, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 1, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 107, Appl
Sequence 19, Appl
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Sequence 33709, A
Sequence 41, Appl
Sequence 40, Appl
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Sequence 2232, Ap
Sequence 1, Appli
Sequence 103, App
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US-10-751-235-54
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US-10-80-813-103
US-10-80-813-103
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ORGANISM: Arabidopsis thaliana
FEATURE:
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Sequence 5, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 26, Appl
Sequence 148190,
                                                                                          January 15, 2006, 13:12:22; Search time 615 Seconds (without alignments) 1035.353 Million cell updates/sec
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2: /cgn2 6/ptodata/1/pubpua/USO9 PUBCCMB.seq:*

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               GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                    nucleic search, using frame_plus_p2n model
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US-10-751-235-7
US-10-751-235-26
US-10-751-235-26
US-10-425-114-32608
US-10-425-115-148190
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Sequence 5, Application US/10751235

Sequence 5, Application US/10751235

Sequence 5, Application US/10751235

Sequence 5, Application OS US20050150002A1

GENERAL INFORMATION:
APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Metabolism in Plants
TITLE OF INVENTION: Metabolism in Plants
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-08604

CURRENT APPLICATION NUMBER: US/10/751,235

CURRENT FILING DATE: 2004-01-02

NUMBER OF SEQ ID NOS: 74

SOFTWARE: Patentin version 3.2

SEQ ID NO 5

LENGTH: 2467
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TIGCAGCCTTATGCAGAAGACGGAAGTGCTGTGAATATGGAAGCGAAGTTCTCTCAGATG
                                       ThrLeuAspValIleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
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; Sequence 7, Application US/10751235

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Sequence 6, Application US/10751235

Sequence 6, Application US/10751235

Publication No. US20050150002A1

GENERAL INCRMATION:
APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Metabolism in Plants
FILE REPRENCE: MSU-08604
TITLE OF INVENTION: Wherebolism in Plants
FILE REPRENCE: MSU-08604
CURRENT REPRENCE: MSU-08604
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74

SOFTWARE: PatentIn version 3.2

SEQ ID NO 6

LENGHH: 4170
Publication No. US20050150002A1
GENERAL INFORMATION:
APPLICANT: DellaPenna, Dean
APPLICANT: Tian, Lia
TIA, Gonyul
TITLE OF INVENTION: Metabolism in Plants
FILE REPERENCE: MSU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT PILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.2
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US-10-751-235-6
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; ORGANISM: Arabidopsis thaliana
US-10-751-235-7
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US-10-751-235-6
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Roya, Thomas J.
APPLICANT: APPLICANT: And Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)8
FILE REFERENCE: 38-21(5322)8
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
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                                                                                      61 LeuLeuProTyrTrpLysIleAspAlaLeuCysLysIleValProArgGln 77
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Matches:
Conservative:
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343.00
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84.42%
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ORGANISM: Zea mays
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US-10-425-115-148190
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US-10-425-114-32608
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US-10-751-255-26

Sequence 26, Application US/10751235
Sequence 26, Application Wolf 10751235
Stubication No. US20050150002A1
Sequence 26, Application No. US20050150002A1
Septication No. US20050150002A1
Septicant: Deliapenna, Dean
Septicant: Tian, Li
APPLICANT: Tian, Li
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Metabolism in Plants
FILE REPERBRICE: MSU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26
SEQ ID NO 26
SEQ ID NO 26
SEQ ID NO 26
SED ID NO 26
SE
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Best Local Similarity:
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; ORGANISM: Zea mays
US-10-751-235-26
Alignment Scores:
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RESULT 10

US-10-437-963-15200

Sequence 15200, Application US/10437963

Sequence 15200, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Bukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21 (53221) B

CURRENT APPLICATION NUMBER: US/10/437,963
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                                                                                                                                               Sequence 24, Application US/10751235
; Sequence 24, Application US/10751235
; Publication No. US20050150002A1
; GENERAL INFORMATION:
; APPLICANT: DellaPenna, Dean
; APPLICANT: Tian, Li
; APPLICANT: Tian, Li
; APPLICANT: Kim, Joonyul
; TITLE OF INVENTION: Novel Carotenoid Hydroxyl
; TITLE OF INVENTION: Novel Carotenoid Hydroxyl
; TITLE OF INVENTION: Novel Carotenoid Hydroxyl
; FILLE REFERENCE: MSU-08664
; CURRENT APPLICATION NUMBER: US/10/751,235
; CURRENT FILING DATE: 2004-01-02
; NUMBER: OF SEQ ID NOS: 74
; SEQ ID NO 24
; LENGTH: 1086
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84.42%
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ORGANISM: Triticum aestivum
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Best Local Similarity:
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| Publication No. US20050150002A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: DellaPenna, Dean
| APPLICANT: Tian, Li
| APPLICANT: Tian, Li
| APPLICANT: Tian, Loonyul
| TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
| TITLE OF INVENTION: Metabolism in Plants
| FILE REPRENCE: MSU-08604
| CURRENT FILING DATE: 2004-01-02
| NUMBER OF SEQ ID NOS: 74
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 25
| LENGTH: 039
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                                                                                       , OTHER INFORMATION: Clone ID: MRT4577_66678C.1
US-10-425-115-148190
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; ORGANISM: Lycopersicon esculentum
US-10-751-235-25
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85.71%
85.75%
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343.00
92.21%
84.42%
87.28%
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 148190
LENGTH: 2537
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Best Local Similarity:
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Query Match:
DB:
                                            TYPE: DNA
ORGANISM: Zea mays
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RESULT 12
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Publication No. US20050150002A1
GENERAL INFORMATION:
APPLICANT: Dellaberna, Dean
APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
                                                                             694 AGTCCTGTTATTGATGCTGTTTACACCGCACTGAAAGAAGCAGGGCTCGTTCTACAGAT 753
       574 CTCGAGACATATGCTTTGAGCGGTGAACCTGTTAATAGGAAGCGAGATTTTCTCAAATG 633
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                                                      21 ThrLeuAspVallleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
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US-10-751-235-22
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Best Local Similarity:
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US-10-751-235-27
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Publication No. US20050150002A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DellaPenna, Dean
APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Tian, Loonyul
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-08604
CURRENT APPLICATION UNDMER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH. 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 ACTITAGAIGIGATIGGITIGICCTIGITCAATTACAATTITGAITCCCTCACATAGAIT 285
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_21066C.1
US-10-437-963-15200
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CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 15200 LENGTH: 1118
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NAME/KEY: misc_feature
LOCATION: (1587)..(1587)
OTHER INFORMATION: n is a,
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ORGANISM: Hordeum vulgare
                                                                                                 TYPE: DNA ORGANISM: Oryza sativa
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Query Match:
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Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 9451

LENGTH: 229
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57.00%
            NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.2
SEQ ID NO 27
LENGTH: 624
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319.00
89.61%
77.92%
81.17%
                                                                   TYPE: DNA
, ORGANISM: Helianthus annuus
US-10-751-235-27
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 CURRENT FILING DATE:
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US-10-424-599-9451
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LeuAspVallleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAspSer 41

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41 SerprovalileGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp 60
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                      ProvalileGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAspLeu
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hydroxylase (LUT1) mRNA, complete cds; nuclear gene for chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Arabidopsis LUT1 locus encodes a member of the cytochrome P450
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Direct Submission
Submitted (30-SEP-2003) Biochemistry and Molecular Biology,
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DellaPenna,D.
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Ilan, L., Musetti, V., Kim, J., Magallanes-Lundback, M. and
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AUTHORS
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   -MODEL-Frame+ p20.model -DEV=x1h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AY424805 Arabidops
AY091083 Arabidops
AF367289 Arabidops
                                                                                 2006, 05:58:40 ; Search time 3652 Seconds (without alignments) 1198.507 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                         LQPYAEDGSAVNMEAKFSQM.....STDLLPYWKIDALCKIVPRQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                 11766282
             GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                      nucleic search, using frame plus pin model
                                                                                                                                                                                                                                                                                hits satisfying chosen parameters:
                                                                                                                                                                                                                                                         5883141 seqs, 28421725653 residues
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Maximum Match 100%
Listing first 45 summaries
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7.0
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AY091083
AF367289
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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15
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9D ln: *
9D lp: *
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1858
3304
                                                                                   January 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenEmbl: *
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Database :

Score

Result ě,

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SAIVALAVFLQRIAVBLQFILNVELVPPQTISMTTGATIHTTNGLYMKVSQR"
                                                                                                                                                    Le , Usaber 1 to Lobo,

Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,

Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,

Tang,C.C., Toriuni,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,

Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,

Jones,T., Kaniya,A., Karlin,Neumann,G., Kawai,J., Kim,C., Lam,B.,

Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,

Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,

Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Direct Submission

Nis Submitted (20-Mar.2002) Plant Gene Expression Center, 800 Buchanan

Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the

collection and clustering of RAFL cDNAs (RAFL cDNA 'RIKEN

Arabidopsis Pull-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,

Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,

Hayashizaki,Y. and Shinozaki,K.
Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A. Arabidopsis Full Length cDNA Clones
Unpublished
2 (bases 1 to 1858)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Annotation is based on the January 2002 version of the Arabidopsis genome submitted to Genbank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /ecotype="Columbia"
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(FLC-1) as a BamHI/KhoI insert."
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9 1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="At3g53130"
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                                                                                          TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                         TITLE
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                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                            AY091083 1858 bp mRNA linear PLN 18-SEP-2002
Arabidopsis thaliana putative cytochrome P450 (At3953130) mRNA,
                                                                                                                                                                                                                                                                                                                                                    /product="chloroplast carotenoid epsilon-ring hydroxylase"
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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaridopsis thaliana

Bukaryota, Viridiplana

Spermarophyta, Banoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 ThrLeuAspVall1eG1yLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 SerProValIleGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 1858)
Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Omodera, C.S., Quach, H.L.,
Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     658 ACACTTCATCATTGGCTTGTCTTTTAACTACAATTTCGATTCTTTGACTACTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LeuLeuProTyrTrpLysileAspAlaLeuCysLysileValProArgGln 77
               State University, East Lansing, MI 48824, USA Location/Qualifiers
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77
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                  thaliana"
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                                                                                                                                                                          chromosome="3"
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Query Match:
DB:
                             Michigan
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VERSION
KEYWORDS
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AUTHORS
                                                                                                                                                                                                                                          gene
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AY091083
                                                                                                                                                                                                                                                                                    CDS
                                                     FEATURES
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3118. .3304
Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M.,
Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H., Southwick, A.,
Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Davis, R.W., Theologis, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       662 ACACTTGATGTCATTGGGTTGTCTCTTTTTAACTACAATTTCGATTCTTTGACTACTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            722 AGTCCTGTCATTGAAGCTGTTTACACTGCTCTTAAAGAAGCTGAGCTTCGTTCTACTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 ThrLeuAspVallleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear PI
BAC clone T4D2,
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Arabidopsis thaliana
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                                                                           and Ecker, J.R.
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Best Local Similarity:
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DB:
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Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowert, L., Carninci, P., Chung, M.K., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin, Neumann, G., Kawai, J., Law, S. Kawi, J., Liu, S. X., Miranda, M., Narusaka, M., Nalwyen, M., Palm, C.J., Pham, P. K., Quach, H.L., Sakano, H., Sakurai, T., Satou, M., Southwick, A. Toriumi, M. Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

Arabidopsis cDNA clones

Unpublished

2 (bases I to 3304)

S Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, L., Carninci, P., Chung, M.K., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin, Neumann, G., Kawai, J., Ishida, J., Jones, T., Kamiya, A., Karlin, Neumann, G., Kawai, M., Lin, J., Liu, S. X., Miranda, M., Narusaka, M., Nayen, M., Lam, L., Liu, J., Luu, S. X., Miranda, M., Narusaka, M., Nayen, M., Seki, M., Southwick, A., Toriumi, M., Yamada, K., Yu, G., Pham, P. K., Quach, H.L., Sakano, H., Sakurai, T., Sahnozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-MAR-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
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Arabidopsis thaliana AT3g53140/T4D2_70 mRNA, complete cds.
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5131. .6090,6168. .6490,6606. .6884,6997. .7249,7359. .7529,
6465. .7737,7816. .7923,8048. .8164,8257. .8346,8438. .8521)
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Weichselgartner, M., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetier, F.
                                                                                                                                              Direct Submission
Submitted (21-DBC-1999) MIPS, at the Max-Planck-Institut fuer
Submitted (21-DBC-1999) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, B-mail:
lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
Coordinator: Marcel Salanoubat and Francis Quetier, Groupement
d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue
Gaston Cremieux, BP191, 91006 Evry Cedex, France;
                                                                                                                                                                                                                                                                                                                                                          http://www.genoscope.cns.fr
information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
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EU Arabidopsis sequencing,project.
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/gene="T4D2.10"
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/gene="T4D2.10"
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BY012891.1 GI:47104306
FLI_CDNA.
Lycoperation esculentum (Solanum lycoperaticum)
SM Lycoperation esculentum
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatorophyta; Magnoliophyta; eudicotyledons; core eudicocyledons; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycoperation.

R I (bases 1 to 1967)
SK ikness, R.F., Wang, W. and Vazeille, A.
Direct Submission and Vazeille, A.
Lycoperation.

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Oryza sativa (japonica cultivar-group) cDNA clone:J013039G17, full
AR065689
                                                                                                                                             PLN 11-MAY-2004
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FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team:,
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Lycopersicon esculentum clone 113997F, mRNA sequence.
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/note="THTDI88"
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SAGSSDFLQNYYRRLLNILLATPDGPADILLASFSSETQNLYERGARRILFSCPED
IITNPTDNGYVPWDGFHPTEAVNBLIAGQLLGQGISLIN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="strong similarity to proline-rich protein, Raphanus sativa, PIR:S16748"
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10124. 10254,10370. 10601)
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Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahadi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Otomo, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosski, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Yoshimura, A., Mitura, J.,
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Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayashizaki, Y.,
Collection, mapping, and annotation of over 28,000 cDNA clones from
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Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakwa, T., Carninoi, P., Fukuda, S., Hanagawi, K., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiranoka, T., Mori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Hiranoka, T., Kanagawa, S., Katch, H., Kawai, J., Kodda, M., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Koda, M., Koya, S., Kuthhara, C., Mattuyama, T., Miyazaki, A., Murata, M., Kakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, H., Sanco, H., Sato, K., Sahai, C., Sakai, K., Sakazume, N., Sanco, H., Sasaki, D., Saro, K., Takahashi, F., Sogabe, Y., Tagami, M., Tagami, T., Tagami, Y., Tagawa, A., Takahashi, F.,
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
Nagate,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (0.5-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@mias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007) This clone is one of the 28K full-length cDNA clones from japonica
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/organism="O<u>ryza</u> sativa (japonica cultivar-group)"
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Tomaru, A., Toya, T., Waki, K.
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Yasunishi,A. and Hayashizaki,Y.
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cioure dentified by a combination of several methods: Gene prediction programs including Genscan and Genscan+ (Chris Burge, http://CCR-081.ntt.edu/GENSCAN.html), GeneMarkHWW (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), FgeneBh (http://genemark.biology.gatech.edu/GeneMark/), FgeneBh (http://www.softberry.com/), and GeneSplicer (Wihaela Pertea and Steven Salzbergy, contact mperteadedigr.org), searches of the complete sequence against a peptide database and the plant EST database at TiGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins are named as prediction programs over most of their length are annotated as prediction programs over most of their length are annotated as hypotherical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.washington.edu/RW/Repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/Repeatmasker.html).
Buell, C.R., Yuan, Q., Ouyang, S., Moffat, K.S., Hill, J.N., Burr, P.C., Hsiao, J., Zismann, V., Pal, G., Bowman, C.L., Fujii, C.Y., VanAken, S.B., Bowman, C.L., Craven, B., Utterback, T.R., Khalak, H., Eddblyum, T.V., Quackenbush, J., White, O., Salzberg, S.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (23-MAY-2002) The Institute for Genomic Research, 9712
Submitted Conter Dr, Rockville, MD 20850, USA, rbuell@cigr.org
On MAY 23, 2002 this sequence version replaced gi:20303636.
Address all correspondence to:rice@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAC clone OSJWBa0001014 is from Oryza sativa chromosome 10
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                  Direct Submission
Submitted (14-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
3 (bases 1 to 178022)
                                                                                                                                                                                                                                                                                                Genomic Research, 9712
                                                                                               Oryza sativa chromosome 10 BAC OSJNBa0001014 genomic sequence
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Submitted (28-AUG-2001) The Institute for Genomic Research, 9
Medical Center Dr. Rockville, MD 20850, USA, rbuell@tlgr.org
6 (bases 1 to 178022)
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Submitted (25-APR-2002) The Institute for Genomic Research, 9
Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org
7 (bases 1 to 178022)
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2 (bases 1 to 178022)
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzae.
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Best Local Similarity:
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                  AP008216 177
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13464 CTTTTACCATACTGGAAGGTAATGTTCCTTTTGCCATGTTATTTTCTAAAAAATCCAATT 113523
/protein_id="AAK20044.1"
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PADTLRRLFAIKITGDNAVDSAGGFICCSVCLQDFRVGEWARRLFSCRHVFHVPCIDC
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                                                                                                                                                                                 complement(20477. .20596)
/rpt_family="Gaijin OB1 MITE element from gb:X52623
4-CL gene for 4-coumarate-CoA ligase (1888 to 2027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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/rpt family-"(GAAAA)n"
complement (24651. .24680)
/rpt family-"AT rich"
complement (27053. .27652)
/rpt family-"GC_rich"
/rpt family-"GC_rich"
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complement(28641. .29130)
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oin(<15036. .15183,15255. .15433,16442. .16525,17234. .17401,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .15433,16442. .16525,17234. .17401,
                                                                                                                                                                                                                                                                                                                                     /protein_id="AAK20056.1"
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RVKIVVGEDELDRIARGVTRRQCAVGSPELLQQQARATEVAAAPMPWRRPESEGGALV
AGRRGEWQPALDGIPEEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (10291. .10434)
/rpt family="Tourist Ol1 MITB element from gb:U72728 Oryza /rpt family="Tourist Ol1 MITB element from gb:U72728 Oryza nonfstaminata receptor-like kinase protein (Xa21), family member P. pseudogene sequence (1080 to 1236) 157 nt" 10300. .10397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="Tourist-like MITE element from O.sativa DNA for LRK2 gene gi|1263159|emb|x89226.1|OSLRK2GEN (1 to 540) 540 nt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5441. .10390
/rpt_family="Tourist-like MITE element from O.sativa DNA
for LRK2 gene gi|1263159|emb|X89226.1|OSLRK2GEN (1 to 540)
540 nt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="Tourist-like MITE element from O.sativa DNA
for LRK2 gene gi|1263159|emb|X89226.1|OSLRK2GEN (1 to 540)
540 nt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="retroelement from gi|5295936|AB026295 Oryza
Bativa (160208 to 165872) 5665 nt"
10278 .10452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Overlap BAC OSJNBa0063E23 (AC113947) has 17 AT repeats in this region." 5433. .5567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      766. 786
/rpt_family="(CGG)n"
3343. 346
/rpt_family="putative Stowaway type MITE element"
complement(3354. 3480)
/rpt_family="putative Stowaway type MITE element"
/rpt_family="putative Stowaway type MITE element"
complement(3808. 3839)
/rpt_family="AT_rich"
complement(3808. 3839)
/rpt_family="AT_rich"
complement(4838. 4871)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5499. .5636
/rpt family="putative Tourist type MITB element"
complement(6712. 6743)
/rpt family="AT rich"
complement(9156. .9226)
                                                                         /note="japonica cultivar-group"
660. .1022
                                                                                                                                                                                                                                                                                                                  product="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="hypothetical protein"
                                                                                                                                                   'note="predicted by genscan+"
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/gene="OSJNBa0001014.22"
/codon_start=1
                                                                                                                                gene="OSJNBa0001014.22"
                                                                                                                                                                               .660. .>1022
'gene="OSJNBa0001014.22"
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4845. 4870
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gene="OSJNBa0001014.25"
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                                                   clone="OSJNBa0001014"
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<14813. .>17815
//locus tag="OSJNBa0001014.12"
//codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (join(<10045. .10997,11698. .11793,12830. .13057, 13670. .13873))
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complement(join(10454. .10997,11698. .11793,12830. .12933))
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VCNLCNVSGHLARECPKSDAINERGGPPPFRGGYSDVVCRACNQVGHMSRDCMAGAFM
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LCGALNLMIDPPVLLVTMKTMCQRETMQNCISMLDQFSSAFKNVHVLTISCMCIVWFL
LYYWQRSYFVEVYHDTSSAIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HHEFTAPIGFAAPYAHWAEVI.ILGIPSFVGPALAPGHMITFMIMIVIRQMEAIETHSG
FDFPPNLTKYIPFYGGAEYHDYHHYVGRQSQSNFASVFTYCDYLYGTDKGYRYHKAYQ
AKMKALGQTEGEKADSNGLSYAKLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPVVFTLAPLPVALLIBLRAPAAVGPPKLQPKVRLSREBFFRCYRDVMRLFFLVIGPLQ
LVSYPTVKNVGIHTGLPLPSLGEMAAQLLVYFLVEDYLNYMIHRLLHGEWGYBKIHRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'translation="MLPYATAAEAEAALGRAMTAAESLWFRYSAGIPDYVLFWHNILF
                                                                                                                                          /note="similar to C 4 sterol methyl oxidase GB:AAC49139 GI:1161339 (Saccharomyces cerevisiae); EST D15076, C97849 from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(<10045. .>13873)
/locus tag="OSJNBa0001014.4"
/note="contains pfam profile PF00098 (zinc finger, CCHC class); EST AU161993, AU057223, AU093006, AU057224 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus tag="OSJNBa0001014.5"
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join(18650. .18935,19046. .19146,19237. .19454,20098.
join(18698. .18935,19046. .19146,19237. .19454,20098.
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INSYPETGLEPAAFAALVPNSADKILGEVIEEIMGDHEMLLLVAGDFSRSCYC"
                                                                                                                                                                                            Join(6954. .7365,7735. .8057,9074. .9221,9316. .9348, 9516. .9818)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative C-4 sterol methyl oxidase"
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This is the pseudomolecule for rice chromosome 10, which was constructed by resolving discrepancies between overlapping BACs, trimming the overlap regions, and linking the unique sequences to form a contigous sequence. Genes in individual BAC clone were identified by a combination of several methods: Gene prediction programs, searches of the complete sequence against a peptide database and EST databases. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with BST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their longth are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Location/Qualifiers)

Location/Qualifiers
                                                                                    113584 TCTGATGTAGCCCTTGTTGTTCTTGATAGATTGTTTGCTGTGCAAGATTGTTCCTAAA 113643
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1702. .1789,1931. .2010,3644. .>3685)
/locus tag="OSJNBa0001014.2"
join(471. .633,699. .781,864. .905,1063. .1104,1442. .1525,
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1702 .1789,1913 .2010,3644 .3685)
/locus_tag="OSJNBa0001014.2"
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RLLRSSPPPEGVPGELMEBEEDSKFVPLNAEDPMYGPPALLLIGFEEGETNKVQFFLR
BLDGEFLKVIHCTEEMTKQTLMDAMHTEQPSIEAVKIAKSMPRICIFSGLTGEEMMF
                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group) chromosome 10, section 71 of AE017117 AE016959
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force="Chromosome Sequence Derivation: nucleotide sequence
in this region was derived from BAC clone OSJNBa0001014
(GB:AC025783)."
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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2 (Dases I to 299735)
Buell, C.R., Wing,R.A., McCombie,W.R., Messing,J. and Yuan,Q. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Rice Chromosome 10 Sequencing Consortium In-depth view of structure, activity, and evolution of rice chromosome 10
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CE (bases 1 to 205408)

CR (chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T. R., Feddblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., Sankiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.

Consortium for Maize Genomics - BAC skim sequencing and assembly Unpublished

L. Diases 1 to 205408)

R. Chases 1 to 205408

R. Chan, A. P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., Sankiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.

Direct Submission

L. Submitted (15-JAM-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr., Rockville, MD 20850

R. Chan, A. D. Dartea, G. Phone, T. C., Chan, A. D. Dartea, G. C., Chan, A. D. Dartea, G. Chan, A. D. C., Chan, A. D. Dartea, G. Chan, A. D. C., Chan, A. D. Chan, A. Chan, A. D. Chan, A. D. Chan, A. Chan
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AC155564
AC155564.2 GI:S8082423
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68822 TCTGATGTAGCCCTTGTTTGTTCTTGATAGATTGTTTGCTGTGCAAGATTGTTCCTAGA 68881
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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68522 CTTGAGACGATCTGCTTTAAGTGGCAAACCTGTAAATATGGAAGCAAGGTTCTCTCAAATG
                                                                                                                                                                                                                                                                               41 SerProvalileGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                         68642 AGCCCTGTTATGATGCTGTTTACACTGCACTCAAGGAAGCAGAACTTCGTTCTACAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 ThrLeuAspVallleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
                                                                                        LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
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           US-10-751-235-1 (1-77) x AE017117 (1-299735)
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Seq_lib_id: ZGEK
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complement (*21629. *22130, 22215. .22396, 22486. .22548,

/note="predicted by fgenesh"

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<30063. .>30866
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/note="similar to cytochrome c type biogenesis protein
CcmE GB:AAF95199 GI:9656598 (Vibrio cholerae)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus tag="OSJNBa001014.6"
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/locus_tag="OSJ
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Location/Qualifiers 1205408 /organiem="Zea mays" /mol_type="genomic DNA"	/btrain="B73" /db xref="taxon:4577" /c1one="zmmBBc0171N08" /17031802 /estimated length=unknown 46634762 /estimated length=unknown /1194811647	/estimated_length=unknown 15559. 15658 /estimated_length=unknown 18073. 18172	/estimated_length=unknown 2271623815 /estimated_length=unknown 3544735546 /estimated_length=unknown	5987659975 /estimated length=unknown 6176261861 /estimated length=unknown 6411464213	/estimated_length=unknown 6825368352 /estimated_length=unknown 7163671735 /estimated_length=unknown 7435274451	/451579044 /estimated length=unknown /estimated length=unknown 8299983088 /estimated length=unknown 8425884357	/estimated_length=unknown 88369. 88468 103421. 103520 /estimated_length=unknown 111901. 112000 /estimated_length=unknown 111901. 112000 /estimated_length=unknown 139115. 139614	/estinated length=unknown 141413. 141512 /estimated_length=unknown 146334. 146453 /estimated_length=unknown 150399. 150498 /estimated_length=unknown 152461. 152560 /estimated_length=unknown 153780. 153879 /estimated_length=unknown 167813. 167911		8.48e-18 Length: 205408 227.00 Matches: 49 80.88\$ Conservative: 6
FEATURES	gap gap gap	•	dap gap	ជុំ		a, a	để đ	gap gap gap gap gap	gap gap gap gap ORIGIN	Alignment Scores: Pred. No.: Score: Percent Similarity:
site:	NOTE: This Consists of is not kno arbitrary. runs of N, This recor as soon as	De preserved.  1 1702: contig of 1702 1703 1802: gap of unknown 1803 4662: contig of 2860 4663 4762: gap of unknown	11547: 11647: 15558: 15658:	18073 1872: gap of unknown 18173 22715: contig of 4543 22716 22815: gap of unknown 35446: contig of 1263 35447 35546: qap of unknown 35546: qap of unknown	35547 59875: contig of 2432 59876 59975: gap of unknown 59976 61761: contig of 1786 61861: gap of unknown 61862 64113: contig of 2552	64114 64213: gap of unknown 64214 68252: contig of 403 68353 68352: gap of unknown 68353 71635: contig of 3283 71636 71735: gap of unknown 71736 74551: contig of 2616 7455 74451: gap of unknown	74552 74915: 989 of unknow 74452 78945 contig of 44767 78945 79044: gap of unknow 82988 contig of 399 83088 84257: contig of 116 84258 84357: gap of unknow 84358 84368: contig of 401 88359 98468: gap of unknow 84358 88369 of wuknow 84358	of 1495 of 8380 on 8380 unknown of 2751 of 1798 unknown unknown of 1843	150499 152460: contrig of 192 152461 152560: gap of unknot 1523780: contrig of 123 153780: 153879: contrig of 123 157810: 167812: contrig of 133 167913: 167912: gap of unknot 170603: 170702: gap of unknot 170703: 198608: contrig of 27 198709: contrig of 27 198709: contrig of 27 198709: contrig of 27 198709: contrig of 27	201018 201117: gap of unknown 201118 204279: contig of 3162 204280 204379: gap of unknown 204380 205408: contig of 1029

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of CR954201 from base 800001 (CR954201 Ostreococcus tauri strain
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Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
                                                                                                                                                                                                                                                                                                                                                                                                                                         ARUDE163 OLYZA SALÍVA (japonica cultivar-group) CDNA clone: 0013135B04, full insert sequence.
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PLI_CONA, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 ThrLeuAspVallleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
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211.00
68.83%
53.25%
53.69%
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CR954201_08
CR954201_09
CR954201_10
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                                                                                                                                                        LeuGlnProTyrAlaGluAspGlySerAlaValAsnMetGluAlaLysPheSerGlnMet
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Analysis Group. Y., Iida, Y.,
FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imctani, K., Ishikawa-Hirozane, T., Kojima, Y., Konho, H., Kouda, M.,
Kishikawa-Hirozane, T., Kojima, Y., Konho, H., Kouda, M.,
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Nakamura, M., Nishi, K., Nomura, K., Nimasaki, R., Ohno, M., Oato, N.,
Saasaki, D., Sato, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sogabe, Y., Tagami, M., Tagami, Takaka, T., Toya, T., Waki, K.,
Yasunishi, A., and Hayashizaki, Y.
URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Pull-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mailskikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
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from base 300001 (CR954209 Ostreococcus tauri strain O
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1 (bases 1 to 2038)
1 Lee, K.-I. and Kim, S.-U.
Direct Submission
Direct Submission
Submitted (18-APR-2004) School of Agricultural Biotechnology, Seoul National University, 7111 Bio Hall, 200BD, Shillim-dong, Kwanak-Gu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AY601887 24-MAY-2004 Ginkgo biloba putative 9782-like cytochrome P450 mRNA, complete
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ThrieudspyallleGlyLeuSerLeuPheAsnTyrAsnPheAspSerLeuThrThrAsp
                                                    41 SerProValileGluAlaValTyrThrAlaLeuLysGluAlaGluLeuArgSerThrAsp
               999 CCTATACCAACTIGGGAAATACCCATATGGAAAGATATTTCCCCGCGGGCAG 1049
                                                                                                      LeuLeuProTyrTrpLysileAspAlaLeuCysLysileValProArgGln 77
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Seoul 151-742, Republic of Korea Location/Qualifiers
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Length:
Matches:
Conservative:
Mismatches:
Indels: 1.35e-16 201.00 76.12% 59.70% 51.15% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.:

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US-10-751-235-1 (1-77) x AY601887 (1-2038)

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31 AsnTyrAsnPheAspSerLeuThrThrAspSerProValIleGluAlaValTyrThrAla 50 g

51 LeuLysGluAlaGluLeuArgSerThrAspLeuLeuProTyrTrpLysIleAspAlaLeu 70 요 δ

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848 AGATGCTAGTTCCTCGACAA 868

Search completed: January 15, 2006, 14:22:26 Job time : 3726 secs

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Sequence:

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E 2 (Dases I to 92611)

Submitted (21-DEC-1999) MIPS, at the Max-Planck-Institut fuer birect Submission

L Submitted (21-DEC-1999) MIPS, at the Max-Planck-Institut fuer submitted (21-DEC-1999) MIPS, at the Krancis Guetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue gaston Cremieux, BP191, 91006 Evry Cedex, France; http://www.genoscope.cns.fr Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
AF022457 Glycine m Z49263 P. sativum m BT002582 Arabidops AY062675 Arabidops AY062675 Arabidops Continuation (5 of Continuation (9 of AX21212 Arabidops AK0100596 Oryza sat AK066680 Oryza sat AK066680 Oryza sat AK064028 Oryza sat AK064048 Oryza sat AL161540 Arabidops Z97337 Arabidopsis AC124218 Medicago AC124218 Medicago AC124218 Medicago AC124218 Sequence AR432884 Sequence AR459441 Skeletone AK432885 Lotus Continuation (2 of AK432885 Sequence AR45941 Skeletone AK432885 Lotus Continuation (3 of AK432885 Lotus Cortinuation (3 of AK402885 Lotus Co
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana DNA chromosome 3, BAC clone T4D2.
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AR017117 Oryza sat
AK065689 Oryza sat
AK105564 Zea mays
AY15554 Zea mays
AY10517 Arabidops
AY058173 Arabidops
AY058173 Arabidops
AK0668163 Oryza sat
AX15503 Zea mays
AK10517 Arabidops
AK068163 Oryza sat
AK105503 Zea mays
AK1056146 Arabidops
AK1056163 Zea mays
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                GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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AC155503
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Listing first 45 summaries
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Maximum DB seq
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/number=11
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7530. .7644
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/gene="T4D2.20"
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/gene="T4D2.20"
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2081. .2434
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5111. 6090,6168. 6490,6606. 6884,6997. 7249,7359. 7529,
7645. 7737,7816. 7923,8048. 8164,8257. 8346,8438. 8521)
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/note="similarity to KIAA0010 protein, Homo sapiens,
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TGGYSDSSRTIKIFWEVMKGFEPSERCLLLKFVTSCSRAPLLGFKYLQPTFIIHKVSC
DTSLWAAIGGQDVERLPSASTCYNTLKLPTYRRASTWREKLLYAITSNAGFELS"
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YRNLMYVGHYDGDLKELCLDFTVTEEFCGKMSIIELKPGGKDTSVTNENKMOYIHAMA
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/note="similarity to BETA-GALACTOSIDASE PRECURSOR,
Lycoperation esculentum, gb:P48980"
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/gene="T4D2.20"
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/gene="T4D2.20"
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|gene="T4D2.10"
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4306. .4393
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                                                                                      ACAATTTCGATTCTTTGACTACTGATAGTCCTGTCATTGAAGCTGTTTACACTGCTCTTA
                                                                                                                                       AAGAAGCTGAGCTTCGTTCTACTGATCTTCTGCCATATTGGAAGGCAAGTTTCCTGTGTT
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1 (bases 1 to 1620)
1 (bases 1 to 1620)
1 Tanh.L., Musetti,V., Kim,J., Magallanes-Lundback,M. and Dellahenna,D.
The Arabidopsis LUT1 locus encodes a member of the cytochrome P450 family that is required for carotenoid epsilon-ring hydroxylation
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                                                                   GTTGTTTGTTATTCCAAAGGTATGGGAAAAAGCTGAGGAATTTCTGCCTGAACGATTCGA
                                                                                                              CATAGATGGCGCAATCCCTAACGAAACAAACACTGATTTCAAGTAAACTCAGTAGAACAC
                                                                                                                          ATCTTTTGACACAAACTACTGAATCAAGATTAGTGGTTTTTGATTAGGGAATTTAAAAGAT
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Submitted (30-SEP-2003) Biochemistry and Molecular Biology,
Submitted University, East Lansing, MI 48824, USA
Michigan State University, East Lansing, MI 48824, USA
1. 1620
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Tian, L., Musetti, V., Kim, J., Magallanes-Lundback, M. and
DellaPenna, D.
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KLETNSSKSQSWVSPDWLTTLTRTLSSGKNDESGIPTANAKLDVADLLGGALFLELY
KWHNEYGPIYTAGDRNPVIVSDPALAKHVLANFYRYAKGLVAEVSEFLFGSGFALA
EGPLWTARRAVDPSLHRRYLSVIVERVFCKCAERLVEKLQPYAEDGSAVWHEAKFSA
VKAERAVDPSLTTDSPVIEAVYTALKEAELRSTDLLPYWKIDALCKIVPRQ
VKAEKAVTLIRETVEDLIAKCKEIVERRGERINDESTVNDADEPSILRETLASREEVSS
VQLRDDLLSMLVAGHETTGSVLTWTLYLLSKNSSALRKAQEEVDRVLEGNNPAFEDIK
BLKYTTRCINESMLVFPPPVLIREAQVPDILLGGNYKVNTGQDIMISVYNIHRSSEVW
BKAEEFLPERFDIDGAIPMETNTDFKFIPF
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                                                                                                                                                                                                                             /product="chloroplast carotenoid
/protein_id="AAR83120.1"
/db_xref="G1:40218379"
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.5%; Score 803; DB 15;
llarity 73.2%; Pred. No. 4.7e-182;
Conservative 0; Mismatches 0;
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1681 TCTCTAATTATTCATGAACTAAATTTTCTGATTGATTTGTTTCCTGGTAGGTCTTGATAA 1740
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EAIVALAAVFLQRLNVELVPDQTISMTTGATIHTTNGLYMKVSQR"
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   a modified pBluescript vector insert."
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                                                                                                                                                                                                                                                                                                                                        Length 1858
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0; Mismatches 0;
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ce="This clone is in
7-1) as a BamHI/XhoI
.1858
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1842
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Best Local Similarity 73.2%;
Matches 1347; Conservative
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3118 . 3304
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Pred. No. 4.3e-182;
0; Mismatches 0;
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Best Local Similarity 73.2%;
Matches 1347; Conservative
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E 10ases 1 to 3304)
Shinn,P., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Banh,J., Bowser,L., Carninci,P., Chung,M.K., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.W., Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Seki,M., Southwick,A., Toriumi,M., Yamada,K., Yu,G., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
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                                                                                                                                                                                                                                                                                                                                         AF367289 3304 bp mRNA linear PLN 24-MAY-2001
Arabidopsis thaliana AT3953140/T4D2_70 mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-MAR-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN arbidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, B., Meyers, M.C., Tracy, S. B., Banh, J. Bowser, L., Chung, M.K., Goldsmith, A.D., Jones, T., Karlin-Neumann, G. Lam, B., Lee, J.M., Lin, J., Liu, S.K., Miranda, M., Nguyen, M., Palm, C.J., Pham, P.K., Quach, H.L., Shano, H., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Davis, R.W., Theologis, A.,
                                                                                                            1288 GAAGAGCTCAAGTTCCTGACATTCTTCTTGGGAACTATAAGGTCAATACCGGACAAGACA
                                                                        GAAGAGCTCAAGTTCCTGACATTCTTCCTGGGAACTATAAGGTCAATACCGGACAAGACA
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|chromosome="3"
|clone="RAFL09-13-P07(R12236)"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Query Match 10.9
Best Local Similarity 68.2
Matches 557; Conservative
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                                                                                                                                                          Arabidopsis thaliana gene for Cytochrom P450 -like protein, partial AK220829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-MAR-2005) Motoaki Seki, RIKEN Genomic Sciences Submitted (12-MAR-2005) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (B-mail:mseki@gsc.riken.jp/, 10-181-45-503-9625, Pax:81-45-503-9586)

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145).

This clone is in a modified pBluescript vector.

Please visit our web site (http://rarge.gsc.riken.jp/) for further
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vtliretvedliakckeivergerindebyvndadpsilrfilasreevssvolrdd
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rcinsmrlyppppuliracypdildpgnykvntgodimisvynihrssevwekaefe
liperpildalpnetydpkeipfsgprkkcygdofalmeaivalakeuvelup
dotismttgatihttinglymkvsor"
                                                                                                                                                                                                                                                                                                                                                                                        Totoki,Y., Seki,M., Ishida,J., Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Shin-i,T., Nakagawa,M., Sakamoto,N., Oishi,K., Kohara,Y., Kobayashi,M., Toyoda,A., Sakaki,Y., Sakurai,T., Iida,K., Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K. Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1077)
TotoKi,Y., Seki,M., Ishida,J., Nakajima,M., Enju,A., Kamiya,A.,
Narusaka,M., Shin-i,T., Nakagawa,M., Sakamoto,N., Oishi,K.,
Kohara,Y., Kobayashi,M., Toyoda,A., Sakaki,Y., Sakurai,T.,
Akiyama,K., Satou,M., Toyoda,T., Konagaya,A., Carninci,P.,
Kawai,J., Hayashizaki,Y. and Shinozaki,K.
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/product="Cytochrom P450 -like protein"
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/db_xref="GI:62319017"
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/mol_type="mRNA"
/db_xref="taxon:3702"
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/note="common name: thale cress"
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Arabidopsis thaliana (thale cress)
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/clone="RAFL22-34-N18"
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                                                                                    361 CAAGCAGAGAAGAGGTTT 378
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   193 AGAGAAGGCGAAAGAATCAATGATGATGAGAGAGTATGTAAATGATGCTGACCCCAAGTATCCTG
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Lycopersicon esculentum clone 113997F, mRNA sequence.
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Lycopersicon esculentum (Solanum lycopersicum)
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Score 268.6; DB 1
Pred. No. 1.8e-53;
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                                                                 0; Mismatches
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1046 TGTAAGATAGTCCCGAGACAGGTGAAAGCTGAAAAGGCTGTAACTTTGATAAGGGAAACT
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                                    TAGTCCTGTCATTGAAGCTGTTTACACTGCTCTTAAAGAAGCTGAGCTTCGTTCTACTGA
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   asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 1967)
Kirkness, E.F., Wang, W. and Vazeille, A.
Direct Submission
Submitted (11-MAY-2004) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20850, USA
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crouse were identified by a combination of several methods: Gene prediction programs including Genscan and Genscan+ (Chris Burge, http://CRc.081.mit.edu/GENSCAN.html), GeneMarkHWM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMarkh), Fgenesh (http://www.softberry.com/), and GeneSplicer (Wihaela Pertea and Steven Salzberg, contact mperteaddig.corg), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins are named at proteins over named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction proteins over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/Repeatmasker.html).
                                                                          Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Entartophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoidaee; Oryzae; Oryza.

1 (bases 1 to 178022)
Buell, C.R., Yuan, O., Ouyang, S., Moffat, K.S., Hill, J.N., Burr, P.C., Hsiao, J., Zismann, V., Pai, G., Bowman, C.L., Fujii, C.Y.,
VanAken, S.B., Bowman, C.L., Craven, B., Utterback, T.R., Khalak, H.,
Feldblyum, T.V., Quackenbush, J., White, O., Salzberg, S.L. and
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Submitted (23-MAY-2002) The Institute for Genomic Research, 9712
Submitted Carter Dr. Rockville, MD 20850, USA, rbuell@tigr.org
MAY 23, 2002 this sequence version replaced gi:20303636.
Address all correspondence to:rice@tigr.org
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Submitted (14 MAR-2001) The Institute for Genomic Research, 9712
Submitted Lorder Dr. Rockville, MD 20850, USA
4 (Dases I to 178022)
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Unpublished
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Submitted (28-AUG-2001) The Institute for Genomic Research, <sup>§</sup>
Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org
6 (bases 1 to 178022)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-MAR-2000) The Institute for Gamedical Center Dr. Rockville, MD 20850, USA (bases 1 to 178022)
AC025783.10 GI:21104901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 178022)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rect Submission
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1331 bp sequence identical to E. coli transposase GB:S67119

AC025783 178022 bp DNA linear PLN 23-MAY-2002 Oryza sativa chromosome 10 BAC OSJNBa0001014 genomic sequence,

RESULT 9
AC025783
LOCUS
DBFINITION

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/hote="predicted by genscan"
join(c15036. .15183,15255. .15433,16442. .16525,17234. .17401,
17688. .>17880)
/gene="OSJNBa0001014.25"
join(15036. .15183,15255. .15433,16442. .16525,17234. .17401,
17688. .17810)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72465. .22516

/ Tpt family="(GAAA)n"

complement(23182. .23375)

/ Tpt family="Rice ROS081X19 insert DNA with repeat units R1-R6 gi|20362|emb|X55420.1|OSRSR1R6"

complement(23216. .2335)

complement(23216. .2335)

/ Tpt family="DNA fragment containing the junction of AA genome-specific tandem repeat sequence TrsA (telomere-associated) gi|804936|dbj|D16452.1|RICTRSA1 Rice (0.sativa), TrsA1 Locus"

/ Tpt family="AT rich"

complement(23490. .23515)

/ Tpt family="(CGG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113262 TGCTGAGAGATTAGTGGAGAAGCTTGAGACATCTGCTTTAAGTGGGAAACCTGTAAATAT 113321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113142 Araaricricringircaacrracacrrdrirriggraricrigrrcaggradgregacgreagr 113201
                                                                                                                                                                                                                                                                               /tränslation="MDASPSSSSSPVAPEVVQWAGGADGFGSAAIGFACRVLCAVAT
VPRAVGSVVGAVTGSAIGLATESGWLRGAGIGAISGAVFSIEVAESSRDLWHSSDSA
VWCLVYWVDIISSLLSGRLVREKVGPAVQSAVQSQLGAISSPFAETSDLFETGGTKGL
PADTLRRLPAIKITGDNAVDSAGEPICCSVCLQDFRVGEMARLPSCRHVFHVPCIDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               785 GGAAGCGAAGTTCTCTCAGATGACACTTGATGTCATTGGGTTGTCTTTTTTAACTACAA 844
                                                                                                                                                                                                                                                                                                                                                                                                 complement(20477. .20596)
/rpt_family="Gaijin_O81 MITE element from gb:X52623 Rice
4-CL_gene for 4-coumarate-CoA ligase (1888 to 2027) 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      665 GGTTCCATCGCTTCACAGGAGGTATTTGTCTGTGATTGTGGAGAGAGTATTCTGCAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCAGAGAGGCTTGTTGAGAAGTTGCAGCCTTATGCAGAAGACGGAAGTGCTGTGAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 605 ATCTTCTCTATTGGGCTTAGCTGAAGTCTGATTTTTTACATAGGCGAGGCGTAGAGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; Length 178022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 239.6; DB 15; Length
Pred. No. 9.3e-47;
0; Mismatches 204; Indels
                                                                                                                                                                                                         /product="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24521. .24618
/rpt_family="(GAAAA)n"
comploment (24651. .24680)
/rpt_family="AT_rich"
complement (27603. .27652)
/rpt_family="GC_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (23942. .24112)
/rpt family="(CGG)n"
complement (24108. .24214)
/rpt_family="(AGGGGG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (24234. .24404) /rpt_family="(CGG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(CCGCG)n"
complement(28641. .29130)
                                                                                                                                                                                                                                 /protein_id="AAK20044.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .24031
family="(CCGCG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .27833
family="(CCGCG)n"
                                                                                                                                                                                                                                                                                                                                                                              WLVRHGSCPLCRRDI"
                                                                                                                                                                                     codon_start=1
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Best Local Similarity 63.2°
Matches 425; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein id="AAK20056.1"
/db xref="c01:13357259"
/tanslation="MTPPNPWGCFPPRSTHRRQPLRHGGGGGVTVVVSRGGGGGAA RVKIVVGBDELDRIAGVTRRQCAVGSPELLQQQARATEVAAAPMPWRRPESEGGALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (10291. .10434)
/rpt family="Tourist Oll MITE element from gb.U72728 Oryza /rpt family="Tourist Oll MITE element from gb.U72728 Oryza longIstaminata receptor-like kinase protein (Xa21), family member F, pseudogene sequence (1080 to 1236) 157 nt" 103300. .10397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5441. .10390
/rpt_family="Tourist-like MITE element from O.sativa DNA
for LRK2 gene gi|1263159|emb|x89226.1|OSLRK2GEN (1 to 540)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'rpt_family="Tourist-like MITE element from O.sativa DNA
:or LRK2 gene gi|1263159|emb|X89226.1|OSLRK2GEN (1 to 540)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="Tourist-like MITE element from O.sativa DNA or LRK2 gene gi | 1263159 emb | X89226.1 | OSLRK2GEN (1 to 540)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5499. ..5636
/rpt_family="putative Tourist type MITE element"
complement(6712. ..6743)
...complement(9156. ..9226)
...complement(9156. ..9226)
...complement(160208 to 165872) 5665 nt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Overlap BAC OSJNBa0063E23 (AC113947) has 17 AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt family="putative Stowaway type MITB element"
complement(3354. .3480)
/rpt family="putative Stowaway type MITB element"
complement(3808. .3839)
/rpt family="AT rich"
complement(3937. .3963)
/rpt family="AT rich"
complement(4838. .4871)
/rpt family="AT rich"
                                              overlaps with rice BAC OSJNBa0063E23 (AC113947) and
                                                                                                                                          (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt family="putative Tourist type MITE element"
10324. .10474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="putative Tourist type MITB element"
complement(12414. .12457)
/rpt_family="AT_rich"
15036. .17810
                                                                                                                                                                                                                                                                               /clone="OSJNBa0001014"
/note="japonica cultivar-group"
                                                                                                                                                                                                                                                                                                                                                                              'note="predicted by genscan+"
GI:455674 has been cut from this BAC.
                                                                                                                                                                                                                                                                                                                                                                                        <e60. .>1022
/gene="OSJNBa0001014.22"
/gene="OSJNBa0001014.22"
/gene="OSJNBa0001014.22"
/codon_start=1
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_tref="taxon:39947"
/chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeats in this region."
                                                                                                                                                                                                                                                                                                                                                   /gene="OSJNBa0001014.22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           766. .786
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3343. .3469
                                                                 OSJNBa0082M15 (AC020666).
Location/Qualifiers
                                                                                                                                                                                                                                                         /map="near C809"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nt"
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complement (join (10454. .10997,11698. .11793,12830. .12933)) /locus tag="OSJNBa0001014.4" /codon_start=1
                                                                                                                                                                                                                                                                                                 /locus tag="OSJNBa0001014.2"
/notas tag="OSJNBa0001014.2"
/not(431. 10.33,699. .781,864. .905,1063. .1104,1442. .1525,
1702. .1789,1913. .2010,3644. .>3685)
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/notas tag="OSJNBa0001014.2"
/locus tag="OSJNBa0001014.2"
/locus tag="OSJNBa0001014.2"
/codon_start=1
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13670. .13873)}
/locus_tag="GSJNBa0001014.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MLPYATPABABAALGRAWTAABSLWFRYSAGIDDYVLFWHNILF
LFVVFTLAPLPVALLELRAPAAVGPFKLQPRVRLSRBEFRCYRDVWRLFFLVJGPLO
LIVSYPTVROVGIHTGLPLPSHGBMAADGLLVYFLVBDYLLNYWIHRLLHGBWGYEKIHRV
HHBFTAPIGFDAPYAHWAEVLILGIPSFVQFALAPGHNITFWLWIVLRQMBALETHSG
RDFPRNLTKYI PFYGGABYHDYHHYVGRQSQSNFASVFTYCDYLYGTDKGYRYHKAYQ
AKWKALGQTEGERADSNGLSYAKLD
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krchfardcpnvalchacglpghiaaecsskolcmnckepghmanscpnegicrncg
ksghiarecsappmlpgemrlcsncykpghlaaectnekacnncrksghlarncpnep
vcnlcnvsghlarecpksdainerggpppfrcgysdvvcracnQvghmsrdcmagafm
                                                                                                                                                            /note="Chromosome Sequence Derivation: nucleotide sequence
in this region was derived from BAC clone OSJNBa0001014
(GB:AC022783)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="ymmamatpuvillersatillersrsprasacvimporrerry
rilrssppppegvpgelmbebedskfvplnaedpmygppaliligfeegetnkvgeflr
blogeflkvihctbemtkgtimdamhtegpsibavkiaksmpricifsgltgeemmp
insypbtglepaafaalvpnsadkilgevibeimgdhemlilvagdfsrscyc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <6954. .>9818
Locus tag="GSJNBa0001014.3"
/note="similar to C 4 sterol methyl oxidase GB:AAC49139
/note="similar to C 4 sterol graph oxidase GB:AAC49139
GI:1161339 (Saccharomyces cerevisiae); EST D15076, C97849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(<10045. .>13873)
/locus tag="OSJNBa0001014.4"
/note="contains pfam profile PF00098 (zinc finger, CCHC class); EST AU161993, AU057223, AU093006, AU057224 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .8057,9074. .9221,9316. .9348,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .9221,9316. .9348,
organism="Oryza sativa (japonica cultivar-group)"
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/codon_start=1
/product="putative C-4 sterol methyl oxidase"
/protein id="AAP54879.1"
/db_xref="GI:31433360"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="putative zinc finger protein"
protein id="AAPS4880.1"
db_xref="GI:31433361"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join (6954. 7365,7735. .8057,9074. 9516. .9818)
/locus tag="0SJNBa0001014.3"
join (7036. .7365,7735. .8057,9074. 9516. .9587)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product="unknown protein"
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'db xref="G1:31433359"
                                     /mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                      xref="taxon:39947
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantee, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae;
1 (bases 1 to 299735)
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                 TTTCGATTCTTTGACTACTGATAGTCCTGTCATTGAAGCTGTTTACACTGCTCTTAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                 -GAGGGTTTGGTTTTTTTTCAGATCGATGC
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2 (bases 1 to 299735)
Buell, C.R., Wing, R.A., McCombie, W.R., Messing, J. and Yuan, Q. Direct Submission
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                                                                                                                                                  AGCTGAGCTTCGTTCTACTGATCTTCTGCCATATTGGAAGGCAAGTTTCC-
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TITIGATICCCTCACATCAGATAGCCCTGTTATTGATGCTGTTTACACTGCACTCAAGGA 68679
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                                                                                                                  /product="putative cytochrome c-type biogenesis protein"
| protein | de AAPS4885.1"
| db xref="di:143386" |
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| DQLVFYLTPTPALASYATDRSKSVRLGGSVALRGSVAHPSASSSEIBFVVTDLTDVL
VRYEGALPDLFREGHSVVVEGFLKPPTDDLRRDTAGRKVSDKARDCECFFSATEVLAK
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Pred. No. 8.7e-47;
0; Mismatches 204; Indels 43; G
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:aq="OSJNBa0001014.23"
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                                                                                              /codon_start=1
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Countement (*21629...*25832)

/locus tag="OsJNBa000104.13"
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                                                                                                                                                                                 RELYCTADPTPATSPPRLETTVCFYLYWVKRKKVVTDLSRRKIRTESIDLAQLVEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="Marpgsgnipgsaciplilililililipseaqopspgyypskmp
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MRFHWPDPTAGFHYALLWPDQILFLYDDVPIRRYEKKVBGTFPEREMWAYGSIWD
ASDWATDGGRYRADYXYQPPV8RFADLKVGGCATAAPPACSSPVPASSGGGSAALISPQQ
RAAMAWAQRNAMVYYYCQDYSRDHTFYPEC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MEERGDEEGGGIRLGGYGDGADGEEBYARGYVAPQVLELSSSS
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SYPNNDLERGYLSLERERNESLERKONOSLYQEINEHTKROI ILCONFINESSLKRINFF
LDGARVMGIDASSQIILTSGRAPGIGARHVLTKAPGWSCSGDQNSPNHIYAGLQNGML
LITPDIRGYPAPLHSWMGLSTHYPHTIHSYVDGGSRKVISASSIGPCTWDVGSRNRP
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WRLPSLQTFADLRPHRQPILDLRFASSSTGERYLGCLSEDRLQVFRVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="MARSVSVSAAKLLAMARSNPRVAIIDVRDEERSYQAHIGGSHH
FSSRSFAARLPELARATGDKDTVVFHCALSKVRGPSGAKMFSDYLSETKEBSGTKNIM
VLERGFNGWELSGQPVCRCTDAPCKGTCSPEEPEL"
<30063. .>30866
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GB:AAF95199 GI:9656598 (Vibrio cholerae)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .28744)
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/note="EST BE039986 from this gene"
/locus tag="OSJNBa0001014.6"
/locus tag="OSJNBa0001014.6"
join(26826. .26911,27026. .27164,28556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="putative cellulase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus_tag="OSJNBa0001014.23"
/note="similar to cytochrome o
                                                                                                                                                                                                                                                                                                                             tag="OSJNBa0001014.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAP54882.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein_id="AAP54884.1"
db_xref="GI:31433365"
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Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiracka, T., Hori, F., Iida, J., Imamura, K., Imoteni, K., Ishii, Y., Itoh, W., Kayaa, J., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Ohno, M., Osa, X., Saitoh, H., Sakai, K., Sakashi, K., Sakazume, N., Nishi, K., Sakai, K., Sakazume, N., Nishi, K., Sakai, K., Sakazume, N., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Saitoh, H., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, T., Sagabi, Y., Tagami, M., Tagawa, A., Takahashi, F., Yasunishi, A., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1127 TGTAAAGAAATTGTCGAAAGAGAAGGCGAAAGAATCAATGATGAGGAGTATGTAAATGAT 1186
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Zea mays strain B73 clone ZMMBBC0171N08, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1067 GTGAAAGCTGAAAAGGCTGTAACTTTGATAAGGGAAACTGTTGAAGACCTTATTGCTAAG 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          947 AAGITICCIGIGITITITICIGIGGITIGITGAITGIGGAACAACITGGAITCITGITAA 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1007 TTGAGAGGGTTTGGTTGTTTTTTTCAGATCGATGCATTGTGTAAGATAGTCCCGAGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       707 GAGAGTATTCTGCAAAATGTGCAGAGAGGCTTGTTGAGAAGTTGCAGCCTTATGCAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                746 IGGCAAACCIGIAAAAIAIGGAAGGAAGGTICICICACAAAGACITIAGAIGACITIGGITI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCTCTTTTTAACTACAATTTCGATTCTTTGACTACTGATAGTCCTGTCATTGAAGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           686 cadacirririroraangigecidagaarragiggadaagerrgagacaredeerrhag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.4%; Score 183; DB 15; Length 1876;
61.8%; Pred. No. 6.6e-33;
ive 0; Mismatches 135; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1187 GCTGACCCAAGTATCCTGCGTTTCTTGCTAGCAAGCAGAAGAGGT 1233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="J013039G17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 61.8
Matches 363; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agrobiological Science Rice Full-Length cDNA Project Team:,
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Dol,K.,
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Dol,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahaqi,W., Suzuki,K., Li,C.,
Kojima,K., Namiki,T., Ohneda,E., Yahaqi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of Interational
Science Genome Sequencing & Analysis Group, Otomo,Y., Murakami,K.,
Ida,Y., Sugano,S., Fuljimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Mazuno,K., Yokomizo,S., Nikkura,J.,
Kusunsaki,T., Sugiyama,A., Mizuno,K., Yokomizo,S., Nikkura,J.,
Kusunsaki,T., Oka,M., Kawamata,M., Yokomizo,S., Nikkura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., Riken,
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Kagawa,I., Kondo,S., Komno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
L. Science 301 (5631), 376-379 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lages 1 to 18/0, Azawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, Hashizume, W., Fujimura, T., Fukuda, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Iishikawa, M., Itch, M., Kagawa, I., Imotani, K., Ishibiki, J., Ishiki, Y., Ishikawa, M., Itch, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kiuchi, S., Kishikawa, Hirozane, T., Kishimoto, N., Kobyashi, M., Kodam, T., Kojima, K., Kojima, Y., Kojima, Y., Kojima, Y., Kojima, Y., Kojima, Y., Moluza, T., Ii, C., Iu, M., Mauda, H., Matsubara, K., Matsuyama, T., Miyaza, J., Miyazaki, A., Mamiki, T., Marikawai, K., Murakami, K., Muta, M., Oka, M., Ooka, M., Sano, H., Sasaki, D., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Suzuki, Y., Tagama, Takeda, Y., Tagama, Takeda, Y., Tagama, Takeda, Y., Tagawa, A., Takabashi, F., Takaku-Akahira, S., Tanaka, T., Tomatu, A., Yamada, Y., Yamada, Y
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (B-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
                                                                                                                                                AKO65689.1 GI:32975707
FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplancae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto, M.
FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
FAIS Genome Sequencing & Analysis Group: Otomo, Y., Kobayashi, M.,
Kujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
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Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
                        sativa (japonica cultivar-group) cDNA clone:J013039G17, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Rice Full-Length cDNA Consortium, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                         Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
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                                            DEFINITION
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AUTHORS
                                                                                                                    ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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estimated_length=unknown
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/strain="B73"
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clone="ZMMBBc0171N08"
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S chan, A.P., Pertea, G., Zheng, L., Cheung, P., Lee, D., Koo, H.,
Utterback, T.R., Sendblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Eedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J. Eedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Consortium for Maize Genomics - BAC skim sequencing and assembly
Unpublished
Consortium for Joseph S., Chan, P., Fertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
3 (bases 1 to 205408)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Chan, A.P., Pertea, G., Zheng, T., Pebliowarz, P., Fraser, C.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr. Rockville, MD 20850 On Jan 25, 2005 this sequence version replaced gi:57863085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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61861: gap of unknown length
61861: gap of unknown length
61861: gap of unknown length
6413: contig of 24329 bp in length
6413: contig of 2252 bp in length
64213: gap of unknown length
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Seq_lib_id: ZGEK
Web site: http://www.tigr.org/tdb/tgi/maize/
Contact: maize@tigr.org
                          AC155564
AC155564.2 GI:58082423
HTG; HTGS_PHASE1.
Zea mays
Zea mays
     unordered pieces
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LFGBASDRLCQKLDAAALKGBEVEMESLFSRLTLDIIGKAVFNYDFDSLTNDTGVIEA
VYTVLREAEDRSVSFIPVWDIPIWKDISPRQRKVATSLKLINDTLDDLIATCKRMVEB
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pngykslekiorekrraelsariasgaptyrkssppstyknglskigipsnyldfmfd
wtgsdodypkypeakgsigavrnbappiplyelftytggifkltfgpksflivsdpsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-AUG-2002) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim,C.J. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.
Location/Qualifiers
                             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. I (bases I to 1788)

Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hayashizaki, Y., Hsuan, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Quach, H.L., Sakuda, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wallender, E.K., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA : 'RIKEN Arabidopsis Full-Length CDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
   Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z. (bases I to 1788)
Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P., Chan, M., Chang, C.H., Dale, J.M., Deng, J.M., Hayashizaki, Y., Hsuan, W.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Squyen, M., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wallender, E.K., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Kim,C.J., Chen,H., Cheuk,K., Shinn,P., Bowser,L., Chan, M., Chang,C.M., Dale,J.M., Deng,J.M., Heuan,W.W., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Woudrh,H.L., Southwack,A., Tang,C.C., Toriumi,M., Wallender,B.K., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Davis,R.W., Theologis,A., and Ecker,J.R.
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/protein_id="AAM98281.1"
/db_xref="G1:22655378"
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/note="This clone is in pUNI 51"
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Sukaryota; Viridiplantae; Streptophyta;
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/db_xref="taxon:3702"
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Arabidopsis thaliana At1g31800/68069_m00159 mRNA, complete cds.
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65.0%; Pred. No. 1.9e-24;
tive 0; Mismatches 117;
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/estimated length=unknown
152461. .152560
/estimated length=unknown
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146354. 146453
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201018. .201117
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/estimated_length=unknown
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Location/Qualifiers
Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
Onodera, C.S., Palam, C.J., Pham, P.K., Quach, H.L.,
Tang, C.C., Tortumi, M., Yamada, K., Yamamura, Y.,
Davis, R.W., Theologis, A., and Ecker, J.R.
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Eukaryots; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E (bases I to 2017)
S Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
Narusaka, M., Nguyen, M., Ondera, C.S., Palm, C.J., Pham, P.K.,
Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C.,
Toriumi, M., Yamanda, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Davis, R.W., Theologis, A. and Ecker, J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AY058173 2017 bp mRNA linear PLN 04-NOV-2001
Arabidopsis thaliana Atlg31800/68069_m00159 mRNA, complete cds.
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                                                                                                                                                                       701 TGTGGAGAGATATTCTGCAAATGTGCAGAGGCTTGTTGAGAAGTTGCAGCCTTATGC 760
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                                Length 1788;
                             Score 91, DB 15, Length 17
Pred. No. 9e-11;
0, Mismatches 95; Indels
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Arabidopsis thaliana (thale cress)
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                                3.7%;
                         Query Match 3.7
Best Local Similarity 60.9
Matches 148; Conservative
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AUTHORS
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons;
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                                                                                  TGTGGAGAGTATTCTGCAAATGTGCAGAGAGGCTTGTTGAGAAGTTGCAGCCTTATGC
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3.7%; Score 91; DB 15; Length 2017; 60.9%; Pred. No. 8.8e-11; arive 0; Mismatches 95; Indels
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  Query Match
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Matches 148; Conservative
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SOURCE
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The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Koesema,B., Meyers,M.C., Shinn,P., Banh,J. Bowser,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G.,

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881 AGCIGITIACACIGCICITIAAAGAAGCIGAGCITICGITCIACIGAICITCIGCCAIAIIG 940
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                                                                                                                                              8.8e-11;
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                                                                                                      Score 91; DB 1; Pred. No. 8.8e-0; Mismatches
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                                                                                                              3.7%;
/replace=""
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                                                                                                                                                       Similarity
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        l (bases i to 2057)

Cheuk, R., Chen, H., Kim, C.J., Koesema, B., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Kawai, J., Lam, B., Lee, J.M., Lin, J., X., Miranda, M., Kawai, J., Lee, J.M., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Gouch, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriuni, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Arabidopsis DNA clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.
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/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db_Aref="taxon:3702"

/chromosome="1"

/clone="RAFL09-33-D23(R14331)"
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product=nAt1g31800/68069_m00159"
protein_id="AAL08302.1"
/db_xref="G1:15912337"
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CDS
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JOURNAL
REFERENCE
AUTHORS
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                                                     REFERENCE
AUTHORS
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17051, A 17244, A 2102, Ap 3, Appli

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

468, App 11988, A

Sequence Sequence Sequence

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Sequence

Sequence 1, Appli Sequence 92564, A Sequence 92565, A

Sequence 12 Sequence 13 Sequence 1

Sequence Seguence

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APPLICANT: Siminszky, Balazs
APPLICANT: Dewey, Ralph E.
APPLICANT: Dewey, Ralph E.
APPLICANT: Corbin, Frederick T.
TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
NUMBER OF SEQUENCES: 23
NUMBER OF SEQUENCES: C. Bennett
ADDRESSER: Virginia C. Bennett
STREET: PO Box 37428
CITY: Raleigh
STATE: No. 6121512th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
US-08-232-463-14
US-09-949-016-12611
US-09-949-016-12611
US-09-949-016-12017
US-09-662-254B-27
US-09-949-016-1227
US-09-949-016-1227
US-09-949-016-1124
US-09-949-016-1198
US-10-104-047-468
US-09-949-016-11988
US-09-949-016-11988
US-09-949-016-11988
US-09-949-016-11988
US-09-949-016-11988
US-09-949-016-92564
US-08-277-031B-12
US-08-277-031B-12
US-08-277-031B-13
US-08-277-031B-13
                                    09-949-016-14413
09-949-016-200471
                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 27627
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,564
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/08948564
Patent No. 6121512
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BENEER, VIZGATIA C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 5051-
TELECOMMUNICATION INFORMATION:
TELEFAX: 919-854-1400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1831 base pairs
                                                            32392
113966
113967
268449
2078
3150
4312
74177
1584
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
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    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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Sequence 156, App
Sequence 126, App
Sequence 22, Appl
Sequence 22, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 1, Appli
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Sequence 130943,
Sequence 13432, A
Sequence 2813, Ap
Sequence 88266, A
Sequence 88266, A
Sequence 13022, A
Sequence 13002, A
Sequence 13002, A
Sequence 1357, Ap
Sequence 1357, Ap
                                                                                                            January 13, 2006, 00:04:14; Search time 434 Seconds (without alignments) 10104.250 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                          1 atggagtcttcactctttc......tgaaggtgagccaaaggtaa 2467
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/P_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
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Compugen Ltd
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US-09-949-016-15466

US-09-949-016-15432

US-09-949-016-15432

US-09-949-016-1870

US-09-949-016-1870

US-09-949-016-88266

US-09-949-016-88267

US-09-949-016-14221

US-09-949-016-1320

US-09-949-016-1321

US-09-949-016-1321

US-09-949-016-1321

US-09-949-016-1321

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US-09-169-192A-156
US-09-169-1789-156
US-09-806-708B-22
US-09-8021-976-2813
US-09-621-976-2813
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                     1303057 seqs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                  GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Database

Result

Length 1831;

DB 3;

3.0%; Score 73.2;

CDS 20..1747

NAME/KEY: LOCATION:

US-08-948-564-15

Query Match

Sequence

US-09-248-796A-1435 US-08-916-421B-2 US-09-692-570-2 -09-902-540-3557 -09-902-540-1171

58407

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                                                                                                                                                          790 CGAAGTICTCTCAGATGACACTTGATGTCATTGGGTTGTCTTTTTTAACTACAATTTCG
                                                                 730 AGAGGCTTGTTGAGAAGTTGCAGCCTTATGCAGAAGACGGAAGTGCTGTGAATATGGAAG
                                                                                                           612 ATAAGCTTCTTGAAGGAGGGGTTATGATGGACCTGACTCAATTGAATTGGATCTTGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 150, Application US/09615192A

gequence 150, Application US/09615192A

general No. 6410718

GENERAL INPORMATION:
APPLICANT: Blokaberg, Leonard N.
APPLICANT: Blokaberg, Leonard N.
APPLICANT: Havukala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content;
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A

CURRENT PILING DATE: 2000-07-12
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1996-09-11
PRIOR PLING DATE: 1996-09-11
PRIOR PLING DATE: 1996-09-11
SPRIOR PLING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastEEQ for Windows Version 3.0
                     Indels
58.9%; Pred. No. 1.3e-10;
tive 0; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                           910 AGCTTCGTTCTACTGATCTTCTGCCATATTGGAA 943
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    Best Local Similarity 58.9
Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-09-615-192A-156
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Sequence 156, Application US/09169789
Patent No. 6653528
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, 11kka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.100352

US-09-169-789-156

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NAME/KEY: promoter Lichary Location (1)...(1141)
COTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters US-09-806-708B-22
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US-09-806-708B-22/C
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; TILE REFERENCE: 4810-58741
; CURRENT FILING DATE: 2001-04-03
; PRIOR PLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.0
; SEQ ID NOS: 23
; SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1047 GTAAGATAGTCCCGAGACAGGTGAAAGCTGAAAAGGCTGTAACTTTGATAAGGGAAACTG
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                                                                                                                                                                                                                                                                                                                                      Length 404;
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2.0%; Score 49.8; DB 3; Length 1:
Best Local Similarity 10.7%; Pred. No. 0.0007;
Matches 92; Conservative 319; Mismatches 439; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                    Score 57.8; DB 3;
Pred. No. 1.8e-06;
0; Mismatches 72;
CURRENT APPLICATION NUMBER: US/09/169,789
CURRENT FILING DATE: 1990-10-09
EARLIER APPLICATION NUMBER: US 08/975,316
EARLIER FILING DATE: 1997-11-21
EARLIER FILING DATE: 1997-11-31
EARLIER FILING DATE: 1996-09-11
EARLIER FILING DATE: 1996-09-11
EARLIER FILING DATE: 1985
SOFTWARE: PastSEQ for Windows Version 3.0
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                       Matches 101; Conservative
                                                                                                                                                                                                                                                                  ORGANISM: Pinus radiata
US-09-169-789-156
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                  SEQ ID NO 156
                                                                                                                                                                                                                                                   TYPE: DNA
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CTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22
                                                                                                                                                                                                                                   CTTTATCTCCTAAGTAAGGTACCTTAATGTATCTTCTACTTTGCTATGCTAGAGAATTTA 1464
                                                                                                                                                                                                                                                                                                                              CTTGGATGGGAGCTTCTCTGTTCTCATTTACCTCTTCAAATTCTCTATGTTCATAGAACT 1524
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                                                                                                                                       GATCTTCTCTCAATGCTCGTAGCGGGTCATGAAACCACTGGATCTGTCCTCACTTGGACA 1404
                                                                                                                                                                                                                                                                                                                                                                                                                   1638 ATGCGTCTCTATCCTCATCCTCTGTAAGCAATCAAGCTCATCTCTCTAATTATTCATGA 1697
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                                                                                                                                                                    AACATCCATCGTTCTTCCGAGGTACAGTTCTCTTCCTTCTCTCGTCCATAGTATAACATA 1877
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NNYMHAAVITTHIDWCYKTWMNTWYWDMMTTMBITTTRNMTTSTNMTNNNNNMWACTNN
                                                .285 TAATCGAAGCTGATGTTGCATTGTGAGGGTTTTTCAGGTATCAAGTGTGCAGTTACGGGAT
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Patent No. 6784342
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT PILLING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
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Pred. No. 0.001;
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SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH: 1141
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TACAATTTCGATTCTTTGACTACTGATAGTCCTGTCATTGAAGCTGTTTACACTGCTCTT
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                      TELEPAN: (703)836-9300
TELEFAX: (703)683-4109
TELEA: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 712 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: line
IMMEDIATE SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 KKAYYRKTTCYSSKGWIWWKRWKKAWITWWWKKTYYWAATRYWWMCWIKRWRASWWYCW 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 SCMMRRKYAGKSKTSYKSMWMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWYASKKY 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 GTYKKKAMCRIKTKIKKKKKGYMMMYWGWRRSYMAMWIRIWIGYAYYRSMMYWWRYRCWK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 WKYTTWYAKCWTKWKWSWSYWMYWKWYYMKTYWRWRRKKKKKAWWKYWKTWWWWWRYAMW
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CITY: Alexandria STATE: VA A
COUNTRY: USA
Z19: 22313-0299
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2197 GAGGGCCTAGAAATGTGTAGGCGATCAGTTTGCATTG 2234
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                                                                                        APPLICANT: Jobert, S. APPLICANT: Jobert, S. TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REFERENCE: GENSET. 054 FRZ CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEG ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                2.0%; Score 48.8; DB 3;
10.4%; Pred. No. 0.0012;
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Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FARINGER, F.
APPLICANT: FARINGER, F.
APPLICANT: FARINGER, F.
APPLICANT: FALINGER, F.
APPLICANT: FALINGER, F.
CORRESPONDENCES: 52
CORRESPONDENCE ADDRESS:
      Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
                                                                           APPLICANT: Dumas Milne Edwards, J.B
                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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US-08-232-463-14
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Best Local S
Matches 35
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Sequence 1, Application US/08916421B
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco-
; FILE REFERENCE: PB275
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; TILE NEFRENCE: PB275
; TILE NEFRENCE: 1997-08-22
; CURRENT PILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR APPLICATION NUMBER: US 60/024,428
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 AAATGGATGAATGAGTACGGACCCATTTACCGTCTCGCTGCTGGTCCTCGTAATTTCGTA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 CGTCTTTTATCACCAAAAACCCAAATTCACATTCTCCATCAGAATCCTCCATTGAGAAACCC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.9%; Score 46.8; DB 2; Length 7218;
Best Local Similarity 0.8%; Pred. No. 0.015;
Matches 3; Conservative 215; Mismatches 142; Indels 0.
                                                                                                                                                   30472/114 IMMU
PILLING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29, 768
REFERENCE/DOCKET NUMBER: 30472/114 IM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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LENGTH: 1664976
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TYPE: DNA ORGANISM: Methanococcus jannaschii	
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LOCATION: (12822) LOCATION: (12822) OTHER INFORMATION: n equals a, t, c, or	ō
NAME/KEY: misc_feature LOCATION: (28257)(28258)	1
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NAME/KEY: misc_feature LOCATION: (84812)	
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LOCATION: (98239)(98239) OTHER INFORMATION: n equals a, t, c, o	5
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OTHER INFORMATION: n equals a, t, c, or	51
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NAMB/KEY: misc feature LOCATION: (103998) (103998)	
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NAME/KEY: m18C_teature IOCATION: (148948)	
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NAMB/KBY: misc_teature LOCATION: (163385)(163385)	
NEWATION: n equal	50 1
NAME/KEI: M18C_LEGULE LOCATION: (191 <u>9</u> 89)(191989)	
RMATION: n equal	<b>5</b> 5 u
ION: (191995) (191995)	
OTHER INFORMATION: n equals a, t, c, or NAME/KRY: misc feature	51
ION: (231980) (231980)	
OTHEK INFORMATION: n equals a, t, c, or NAME/KEY: misc feature	ס 
LOCATION: (234187)(234187) OTHER INFORMATION: n equals a. t. c. or	Ö
CEY: misc_feature	
LOCALION: (234220)(234220) OTHER INFORMATION: n equals a, t, c, or	50 (
NAME/KEY: misc_feature LOCATION: (234814)(234814)	
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KEY: misc reatur ION: (309398)(	
OTHER INFORMATION: n equals a, t, c, or NAME/KEY: misc feature	<b>5</b> 1.
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NAMATION: n equal	Б.,
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LOCATION: (779455).. (779455)
OTHER INFORMATION: n equals a, t,
NAME/KRY: misc feature
LOCATION: (779676).. (779676)
OTHER INFORMATION: n equals a, t,
NAME/KRY: misc feature
LOCATION: (855539).. (855539)
OTHER INFORMATION: n equals a, t,
NAME/KRY: misc feature
LOCATION: (871619).. (871619) IOCATION: (319226)...(319226)
OTHER INFORMATION: n equals a, t,
NAME/KEX: mlac\_feature
LOCATION: (559167)...(559167)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc\_feature
LOCATION: (559241)...(559241)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc\_feature
LOCATION: (600992)...(600992)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc\_feature NAME/KRY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t,
NAME/KRY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (1130881).
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: nequals a, t,
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LOCATION: (622708).. (622708)
COTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (657081).. (657081)
OTHER INFORMATION: n equals a, t LOCATION: (657081)...(657081)
OTHER INFORMATION: n equals a, t.
NAME/KRY: misc feature
LOCATION: (657203)...(657203)
OTHER INFORMATION: n equals a, t.
NAME/KRY: misc feature
LOCATION: (674435)...(674435)
OTHER INFORMATION: n equals a, t.
NAME/KRY: misc feature
LOCATION: (682442)...(682442)
OTHER INFORMATION: n equals a, t.
NAME/KRY: misc feature
LOCATION: (713652)...(713652)
OTHER INFORMATION: n equals a, t.
NAME/KRY: misc feature
LOCATION: (713652)...(713652)
OTHER INFORMATION: n equals a, t.
NAME/KRY: misc feature
LOCATION: (741684)...(741684) NAME/KEY: misc\_feature\_LOCATION: (1470091) LOCATION: (1470091)..(1470091) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (1569020)..(1569020) OTHER INFORMATION: n equals a, NAME/KRS: misc.feature. LOCATION: (1119881)..(1119881) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1349491)..(1349491) OTHER INFORMATION: n equals a,

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OTHER INFORMATION: n equals a, t,
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LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a,
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LOCATION: (98239) ..(98239)
OTHER INFORMATION: n equals a,
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a,
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LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a,
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LOCATION: (103998)...(103998)
OTHER INFORMATION: n equals a,
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LOCATION: (191989)...(191989)
OTHER INFORMATION: n equals a,
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LOCATION: (163385)..(163385)
JTHER INFORMATION: n equals a,
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THER INFORMATION: n equals a,
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LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals
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LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals
                                                                                                           NAME/KEY: misc feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals
                                   NAME/KEY: misc feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals
INFORMATION: n equals
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NAME/KEY:
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NAME/KEY:
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Patent No. 6797466

GENERAL INFORMATION:
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6797466

TITLE OF INVENTION: Januaschii
FILE REFERENCE: PB275C1
CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT PILING DATE: 1996-08-22
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                  Query Match
1.8%; Score 44.6; DB 3; Length 1664976;
Best Local Similarity 50.2%; Pred. No. 1.4;
Matches 110; Conservative 0; Mismatches 109; Indels 0;
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LOCATION: (1637998)..(1637998)
COTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854)..(1664855)
COTHER INFORMATION: n equals a, t, c, or g
US-08-916-4218-1
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       OTHER INFORMATION: n equals a, t,
                       NAME/KEY: misc feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t
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LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a,
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LOCATION: (28257)...(28258)
OTHER INFORMATION: n equals a,
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals
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LOCATION: (84808)..(84808)
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NAME/KEY: misc feature
LOCATION: (1096846)..(1096816)
OTHER INFORMATION: n equals a, t, c, or
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t,
                                                                       NAME/KEY: misc feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t,
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc feature
LOCATION: (559241). (559241)
OTHER INFORMATION: n equals a, t,
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LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t,
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INFORMATION: n equals a, t,
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LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t,
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LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a,
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a,
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
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GENERAL INFORMATION: J. Craig et al.

PAPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/21,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRASESEQ for Windows Version 4.0

SOFTWARE: PRASESEQ for Windows Version 4.0 1436027 TGAAAAACCTGAAGAGTTGTTCATGGTAAAGGACCAAGAATCATTGTTAAAGAGAGTAG 1436086 1435967 GAGAGAAATGAGCATCAAAGAGAATTAATGGAAATAATTGAAGCAATTAAATATACGTC 1436026 1060 GAGACAGGTGAAAGCTGAAAAGGCTGTAACTTTGATAAGGGAAACTGTTGAAGACCTTAT 1119 1120 ȚGCTAAGTGTAAAGAAATTGTCGAAAGAGAAGGCGAAAGAATCAATGATGAGGAGTATGT 1179 1180 AAATGATGCTGACCCAAGTATCCTGCGTTTCTTGCTTGCAAGAAGAGAGGGTTAAAAC 1239 1863 AAGTGCTGGGAGTATAGGCGTGAGCCACCGTGGCCTGGCCTAGATTCCATTTGTATCTC 1922 829 770 AAGIGCTGIGAATATGGAAGCGAAGTTCTCTCAGATGACACTTGATGTCATTGGGTTGTC Gaps DB 3; Length 1664976; 2; ö Length 43192; 57; Indels 1.8%; Score 44.6; DB 3; Length 1 50.2%; Pred. No. 1.4; tive 0; Mismatches 109; Indels 1436147 GATAAAGGCAAAGATTATTATAAAAAGGCTATAAATT 1436185 1240 TITITICCTIAAGITITATAAGCAAATITIGGCCTTTCATT 1278 DB 3; Ouery Match
1.7%; Score 41.8; Di
Best Local Similarity 59.9%; Pred. No. 1.2;
Matches 88; Conservative 0; Mismatches NAME/KEY: misc feature LOCATION: (1349473)..(1349473) OTHER INFORMATION: n equals a, t, c, or g b or g Ð ö ö or Sequence 15466, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION: LOCATION: (1313224)..(1313224) OTHER INFORMATION: n equals a, t, c, NAME/KEY: misc feature LOCATION: (1310988)..(1310988) OTHER INFORMATION: n equals a, t, c, ΰ NAME/KEY: misc feature LOCATION: (1119881)..(1119881) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1130881)..(1130881) OTHER INFORMATION: n equals a, Query Match 1.8 Best Local Similarity 50.2 Matches 110; Conservative FEATURE: NAME/KEY: misc\_feature RESULT 10 US-09-949-016-15466 TYPE: DNA ORGANISM: Human US-09-949-016-15466 g ò 셤 ઠે 셤 ò Š ઠ

Gaps

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ARENEAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REFERENCE: CL001307
FILLE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASSESQ for Windows Version 4.0
ILENGTH: 67902
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                                                                                                                                                                                                              26889 TTTTTAAGAGTAGCCAAAAGGAGGAGAAACTTAAAAGCAAATTGCCTTAGTAAGGATAA
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                                                                 DB 3; Length 67899;
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19.09-621-976-2813/c
| Sequence -2013, Application US/09621976
| Sequence -2013, Application US/09621976
| Patent No. 6639063
| GENERAL INFORMATION:
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Jobert, S.
| APPLICANT: Giordano, J.Y.
| APPLICANT: Giordano, J.Y.
| TITLE OF INVERTION: ESTS and Encoded Human Proteins.
| FILE REFERENCE: GENSET.054PR2
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Pred. No. 2;
0; Mismatches 61;
                                                                 ; Score 41.4; DB
; Pred. No. 2;
0; Mismatches
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Patent No. 6812339
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                                                                 Query Match 1.7%;
Best Local Similarity 56.1%;
Matches 78; Conservative
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Best Local Similarity 56.1
Matches 78; Conservative
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US-09-949-016-11870
, ORGANISM: Human
US-09-949-016-15432
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Sequence 13043, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERENCE: CLOOKINGOTO

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SOFTWARE: FREAESEQ for Windows Version 4.0

SEQ ID NO 130943
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j Betent No. 6812339

j GENERAL INFORMATION:

j APPLICANT: VENTER, J. Craig et al.

i APPLICANT: VENTER, J. Craig et al.

i TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREETENCY

SOFTWARE: REALESO FOR WINGOWS VERSION 4.0
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                                             1923 igricitalacaalacrititrocicitadaciricadarriticordicoridarcicago 1982
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Pred. No. 0.14;
0; Mismatches 61; Indels
                                                                                                                                                  1983 regacrecreaagaagaaregeeerr 2009
                                                                                                       888 TACACTGCTCTTAAAGAAGCTGAGCTT
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Best Local Similarity 56.1<sup>†</sup>
Matches 78; Conservative
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US-09-949-016-15432/c
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LENGTH: 67899
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FACELIA NO. 1921-239.
FACELIA OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
FRIOR FILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 88266
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                 1904 ATCTTTGTGTGGTTCGGATATCTAACCGGAGTGGACATTCCTAGTATTACATTCATGCCC 1963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 AWGKWKSMRSAMSMCTRMYYKKGSTYWTWKCTCATWCYWYWKYWKRWWSKTCWSGSRGGY 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 MMWYMWWAWCMSSRGAAMYRRTMMMGYRYWWRKKSYRRTRCAWAYAWKTKRSYYWCWRW 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 KWKRCMOMOMMAMAYGKITMMARACWKITRYWRWAMAMWRAMWTMOMYYWYWYWAMKRRWM 30
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1.6%; Score 39.6; DB 3; Length 601;
Best Local Similarity 49.1%; Pred. No. 0.48;
Matches 105; Conservative 0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                   Query Match
1.6%; Score 40; DB 3; Length 832;
Best Local Similarity 8.6%; Pred. No. 0.44;
Matches 28; Conservative 159; Mismatches 139; Indels
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CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
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US-09-949-016-88266/c
Sequence 88266, Application US/09949016
; Patent No. 6812339
                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                    ; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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Search completed: January 13, 2006, 07:19:43 Job time : 438 secs

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US-10-751-235-47
US-10-437-663-37324
US-10-424-599-19723
US-10-425-114-78
US-10-425-115-59515
US-10-425-115-59515
US-10-751-235-46
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Sequence 5, Application US/10751235

Sequence 5, Application US/10751235

Sequence 5, Application US/10751235

Sequence 5, Application US/10751235

Sequence 5, Application US/10751235

GENERAL INFORMATION:
APPLICANT: DellaPenna, Dean
APPLICANT: Aim, Joonyul
TITLE OF INVENTION: Metabolism in Plants
TITLE OF INVENTION: Metabolism in Plants
TITLE OF INVENTION: Metabolism in Plants
TITLE OF INVENTION: Metabolism in Plants
TITLE OF INVENTION: WHOMER: US/10/751,235

CURRENT APPLICATION NUMBER: US/10/751,235

CURRENT PILING DATE: 2004-01-02

NUMBER OF SEQ ID NOS: 74

SOFTWARE: Patentin version 3.2

SEQ ID NO 5 = Instant application 100.0%; Score 2467; 100.0%; Pred. No. 0; tive 0; Mismatches TYPE: DNA ORGANISM: Arabidopsis thaliana -10-751-235-5 Query Match
Best Local Similarity 100.
Matches 2467; Conservative 2467

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Gaps

; 0

DB 9; Length 2467; 0; Indels 9

CCTACGCGTCTTTTATCACCAAAACCCAAATTCACATTCTCCATCAGATCCTCCATTGAG 120

1 ATGGAGTCTTCACTCTTTTCTCCATCTTCCTCTTTACTCTTCTCTCTTCACTGCAAAA

н 61 AAACCCAAACCCCAAACTCGAGACCAATTCATCGAAATCCCAATCATGGGTCAGTCCCGAT 180

121 121

61

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180

ATCGCGAACGCGAAGCTCGACGATGTCGCTGATCTCCTCGGAGGTGCTCTTTTTTACCT 300

241

301

241

CTCTACAAATGGATGAATGAGTACGGACCCATTTACCGTCTCGCTGCTGGTCCTCGTAAT 360

Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Seguence	Sequence
ID	US-10-751-235-5	US-10-751-235-6	US-10-751-235-7	US-10-739-930-773	US-10-425-114-32608	US-10-425-115-148190	-23	US-10-751-235-23	-10 - 424 - 599 - 1	US-10-751-235-22	US-10-437-963-15200	US-10-751-235-27	-10-751-235-2	US-10-751-235-26	US-10-437-963-15203	US-10-424-599-9451	US-10-425-115-77232	-10-424-599-1220	US-10-767-701-31323	US-10-751-235-41	US-10-751-235-40	US-10-751-235-45	US-10-425-114-1109
DB	6	σ	σ	8	7	80	σ	თ	7	σ	7	σ	σ	6	7	7	œ	7	7	9	σ	σ	7
Length	2467	-	2467	3377	1804	2537	8	1638	667	1686	1118	624	839	531	1596	229	478	904	567	1788	2057	1278	1078
A Query Match	100.0	100.0	•	32.5	•	7.9	7.6	7.6	7.5	7.4	7.3	6.9	•	5.9	5.2	4.8	4.7	4.4	3.8	3.7	3.7	٠	3.5
Score	2467	2467	2465.4	803	195.8	σ	187.2	œ	185	183	181	169.6	161	144.6	128.8	118.2	116.8	109.2	93.8	91	91	8.06	87.4
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GAAGAGCTCAAGTTCCTGACATTCTTCCTGGGAACTATAAGGTCAATACCGGACAAGACA 1800
                                                                       1730 AAIGTGCGAGAGAGGCTTGTTGAGAAGTTGCAGCCCTTATGCAGAAGACGGAAGTGCTGTGA
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                                                                                                                                     781 ATAIGGAAGCGAAGTICTCTCAGAIGACACTIGAIGICATIGGGITGICTTTIAACT
                                                                                                                                                                   1790 ATAIGGAAGCGAAGTTCTCTCAGATGACACTTGATGTCATTGGGTTGTCTTTTTAACT
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                                                                                                                                                                                                                                                                                                                                 AAGAAGCTGAGCTTCGTTCTACTGATCTTCTGCCATATTGGAAGGCAAGTTTCCTGTGTT
                                                                                                                                                                                                                                                                                                                                                                       1910 AAGAAGCTGAGCTTCTTCTTCTTCTTCTGCCATATTGGAAGGCAAGTTTCCTGTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTGTATAAACGAGTCAATGCGTCTCTATCCTCCTCTGTAAGCAATCAAGCTCATC
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                                               AATGTGCAGAGAGGCTTGTTGAGAAGTTGCAGCCTTATGCAGAAGACGGAAGTGCTGTGA
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100.0%; Score 2467;
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Matches 2466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	181 TGGCTCACAACACTCGTACCCTTTCCTCAGGAAAAACGACGAGTCAGGTATACCA 24  181 TGGCTCACAACACTCACTCGTTTCCTCAGGAAAAACGACGAGTCAGGTATACCA 24  181 TGGCTCACACACCACCTCTCTTTCCTCAGGAAAAAACGACGAGTCAGGTATACCA 24  241 ATCGCGAACGCGAAGGTCGACGATGTCGCTGATCTCCTCGGAGGTGCTCTTTTTTACCT 30  241 ATCGCGAACGCGAAGCTCGACGATGTCGCTGATCTCCTCGGAGGTGCTCTTTTTTACCT 30  241 ATCGCGAACGCGAAGCTCGACGATGTCGCTGATCTCCTCGGAGGTGCTCTCTTACCT 30	301 CTCTACAAATGGATGAATGAAGACCCATTTACCGTCTGGCTGG	GLIANGE CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROL CON	QY         541 TTGTGGAAGTAATGTGTGACTGTTTGTAAGTAACTCTAATTTTAGGGTTTAGAT         600           Db         541 TTGTGGAAGTAATGTGACTGTCTTGTATGATAACTCTAATTTTAGGGTTTAGAT         600           QY         601 TCCAATCTTCTCTATTGGGCTTAGGTGAAGTCTGATTTTTACATAGGCGAAGGCGTAGAG         660           Db         601 TCCAATCTTCTCTATTGGGCTTAGGTGAAGTCTGATTTTTACATAGGCGAAGGCGTAGAG         660           Db         601 TCCAATCTTCTCTATTGGGCTTAGGTGAAGTCTGATTTTTACATAGGCGAAGGCGTAGAG         660	Qy         661 CGGTGGTTCCATCGCTTCACAGGAGGTATTTGTCTGTGATTGTGGAGAGAGTATTCTGCA         720           bb         661 CGGTGGTTCCATCGCTTCACAGGAGGTATTTGTCTGTGATTGTGGAGAGTATTCTGCA         720           Qy         721 AATGTGCAGAGAGGCTTGTTGAGAAGTTGCAGCCTTATGCAGAAGACGGAAGTGCTGTGA         780           Db         721 AATGTGCAGAAGAGGCTTGTTGAGAAGTTGCAGCCTTATGCAGAAGACGGAAGTGCTGTGA         780           Db         721 AATGTGCAGAAGAGGCTTGTTGAGAAGTTGCAGCCTTATGCAGAAGACGGAAGTGCTGTGA         780	781 781 841		DD 1021 TIGITITITICAGATGGATTGTGTAAGATAGTCCCGAGACAGGTGAAAGCTGAAAA 1080
Qy         1801 TTATGATTTCAGTCTATAACATCGATCGTTCTTCCGAGGTACAGTTCTTCTTCTTCT 1860           Db         2810 TTATGATTCAGTCTATAACATCCATCGTTCTTCCGAGGTACAGTTCTCTTCTTCTCTC         2869           Qy         1861 GTCCATAGTATAACATAGGGAGGCCTAATCTCTCTTCTTCTTTGTGTGTTCGG         1920           Db         2870 GTCCATAGTATAACATAGGGGGCCTAATCCTTCTCTTCT		Oy 2101 ATCTTTGACACAAACTACTGAATCAAGATTAGATTTGATTAGAAGAT 2160	3230 ATCAGTTTGCATTGATGGGGCGATTGTGTGCGCGGGGTTTCTTCTGGCGGTTAACG 2281 TTGAGCTGGTTCCTGATCAGCCATTAGCATGACCACAGGGGCAACCACACACCACA 3290 TTGAGCTGGTTCCTGATCAGACCATTAGCATGACCACAGGAGCAACCATACACCACCA 3290 TTGAGCTGGTTCCTGATCAGACCATTAGCATGACCACACCACCA	Qy 2341 AFGTATGCCAATGTTTCACACTCGAGAGATTAATGAGAGTCTTTGTTTAGAATG 2400	Oy 2461 AAGGTAA 2467	SQUENCE.  Publication No. US20050150002A1  Publication No. US20050150002A1  GENERAL INFORMATION: APPLICANT: Tian, Li APPLICANT: Kim, Joonyul TITLE OF INVENTION: Novel Caroten TITLE OF INVENTION: Metabolism i	FILE REFERENCE: MSU-08604  CURRENT APPLICATION WUMBER: US/10/751,235  CURRENT PILING DATE: 2004-01-02  NUMBER OF SEQ ID NOS: 74  SEQ ID NO 7  LENGTH: 2467  TYPE: DNA  ORGANISM: Arabidopsis thaliana US-10-751-235-7	Query Match 99.9%; Score 2465.4; DB 9; Length 2467;  Best Local Similarity 100.0%; Pred. No. 0;

0y         2161         GATTTTCTTTTTCACCAGATTCATCCATTCAGGGAGGCCTAGAAAATGTGAGGCG         2220           Db         216.1         GATTTTCTTTTTCACCAGATTCATCCCATTCAGGGGCCTAGAAAATGTGTAGGCG         2220           0y         2221         ATCAGTTTGCATTGATGGAGCCAATTGTGGCGGTGTTTCTTCAGGGGTTAAACG         2280           0y         2221         ATCAGTTTGCATTGATGGAGCCAATTGTGGCGGTGTTTCTTCAGGGGTTAAACG         2280           0y         2281         TTGAGCTGGTTCCTGATCAGACCATTAGCATGACCACAGGGCAACCATACACACAC	tion US/10739930  40216190A1  David K.  David K.  PLANTS AND USES THEREOF FOR 1(53377)B  NUMBER: US/10/739,930  2003-12-18  : 11088  thaliana  Clone ID: ARATH-23APR03-CLUST  32.5\$; Score 803; DB 8;	SINITIATILY 73.2%; 7; CONSELVATIVE AIGGAGICTITCACTETITIC AIGGAGICTITTATCACC CCTACGCGTCTITTATCACC AAACCCAAACCCAAACTCGA AAACCCAAACCCAAACTCGA TGGCTACAACACTCATCGA AAACCCAAACCCAAACTCGA TGGCTAACACAACTCGAAATCGAAACTCGA ATCGCGAACGCGAAGCTCGAATCGAA
1081   GGCTGTAACTTTGATAAGGGAAACTGTTGAAGACCTTATTGCTAAGTGTAAAGAAATTGT   1140	141   TACTTTGCTATGCTAGAATTTACTTGGATGGGAGCTTCTCTGTTCTCATTTACCTCTT	1741

Db   1172	REBULT 5  18.10-425-114-32608  18.40-425-114-32608  18.40-425-110 No. U3200400348881  19.40-425-110 No. U320040034881  19.40-425-110 No. U32004  19.40-425-110 No. U32004  19.40-425-110 No. U32004  10.40-425-110 N

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Sequence 24, Application US/10751235
Publication No. US20050150002A1
GENERAL INFORMATION:
APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Tian, Li
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-08604
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24
LENGTH: 1086
                                                                                                                                                                                                           1038 TGTAAAGAAATAGTGGAAGCTGAAAATGAACAGATTGAGGGTGAGGAATATGTAAACGAA 1097
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                                                 1007 TTGAGAGGTTTGGTTTTTTTTCAGATCGATGCATTGTGTAAGATAGTCCCGAGACAG
                                                                                   -----rigigcaagaraarcccaagacag
                                                                                                                                                                                       TGTAAAGAAATTGTCGAAAGAGAGAGGCGAAAGAATCAATGATGAGGAGTATGTAAATGAT
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61.9%; Pred. No. 7.2e-40;
ive 0; Mismatches 138;
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; ORGANISM: Triticum aestivum
US-10-751-235-24
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Matches 369; Conservative
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPRENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/203-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
LENGTH: 2537
                                                                                                                                     1066
                                                                                                                                                                                                       1067 GTGAAAGCTGAAAAGGCTGTAACTTTGATAAGGGAAACTGTTGAAGACCTTATTGCTAAG 1126
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                                                                  AAGTTTCCTGTGTTTTTTTCTGTGGTTTGTTGATTGGAACAATTGGATTCTTGTTAA 1006
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US-10-425-115-148190
                                                                                                   694 TGGTTTC----
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ORGANISM: Zea mays
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US-10-425-115-148190
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Sequence 122968, Application US/10424599
; Sequence 122968, Application US/10424599
; Sequence 122968, Application No. US20040031072A1
; Sequence 122968, Application No. US20040031072A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa Thomas J
    APPLICANT: Cavalic David K
    APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
    TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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    TITLE ACID MOS: 285684
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            1127 TGTAAAGAAATTGTCGAAAGAGAAGGCGAAAGAATCAATGATGAGGGGGGGTATGTAAATGAT 1186
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                                                                                                                                     1187 GCTGACCCAAGTATCCTGCGTTTCTTGCTTGCAAGCAAAGAGATTTAAACTTT 1242
                                                                                                                                                                                               GCAGATCCTAGCATCCTGCGTTTTTTACTTGCTAGCCGTGAAGAGGTCAGCAGTTT 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
7.5%; Score 185; DB 7; Length 667;
Best Local Similarity 69.9%; Pred. No. 2.2e-39;
Matches 283; Conservative 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            458 TTGGTTCGGGTTTCGCTATCGCTGAAGGACCTCTTTGGACAGTAA 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_82046C.1
US-10-424-599-122968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-10-751-235-22
US-10-751-235-22
; Sequence 22, Application US/10751235
; Publication No. US20050150002A1
; GENERAL INFORMATION:
; APPLICANT: DellaPenna, Dean
; APPLICANT: Tian, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                          RESULT 9
US-10-424-599-122968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278
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Sequence 23, Application US/10751235
Sequence 23, Application US/20050150002A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Metabolism in Plants
FILE REPERENCE: MSU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      947 AAGTITCCTGTGTTTTTTCTGTGGTTTGTTGTTGTGGAACAATTGGATTCTTGTTAA 1006
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                                                                                                                        1127 TGTAAAGAAATTGTCGAAAGAGAAGGCGAAAGAATCAATGATGAGGAGTATGTAAATGAT 1186
1067 GTGAAAGCTGAAAAGGCTGTAACTTTGATAAGGGAAACTGTTGAAGACCTTATTGCTAAG 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 887 TIACACTGCTCTIAAAGAAGCTGAGCTTCGTTCTACTGATCTTCTGCCATATTGGAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               714 TTACACCGCACTGAAAGAAGCAGAGGCTCGTTCTACAGATCTTTTACCATACTGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           767 CGGAAGTGCTGTGAATATGGAAGCGAAGTTCTCTCAGATGACACTTGATGTCATTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  474 geneaeacenaeaecaeneneeraecareneraeaaaaanteerereaenaareerea
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                                                                                                                                                                                                                                                                                             940 GCAGATCCTAGCGGTTTTTTACTTGCTAGCCGTGAAGAGTCAGCTTT 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.6%; Score 187.2; DB 9; Best Local Similarity 61.9%; Pred. No. 9.2e-40; Matches 369; Conservative 0; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:

NAME/KEY: misc_feature

LOCATION: (1587)..(1587)

OTHER INFORMATION: n is a, c, g, or t
US-10-751-235-23
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                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-10-751-235-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                827
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Sequence 27, Application US/10751235
Sequence 27, Application No. US20050150002A1
GENERAL INFORMATION:
APPLICANT: Tian, Li
APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MGU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GCTGTTTACACTGCACTCAAGGAAGCAGAACTTCGTTCTACAGATCTTTTACCATACTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ACGAAGGIGAGACGICGAICACITGIACCAICTCIACAAACGAITICICICGGIGAIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  702 GTGGAGAGAGTATTCTGCAAATGTGCAGAGAGGCTTGTTGAGAAGTTGCAGCCTTATGCA 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GTTGACAGAGTTTTTTGTAAATGTGCTGAGAGATTAGTGGAGAAGCTTGAGACATCTGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TTAAGTGGCAAACCTGTAAATATGGAAGCAAGGTTCTCTCAAATGACTTTAGATGTGATT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 GGTTTGTCCTTGTTCAATTACAATTTTGATTCCCTCACATCAGATAGCCCTGTTATTGAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         642 ACATAGGCGAGGCGTAGAGCGGTGCGTTCCATCGCTTCACAGGAGGTATTTGTCTGTGATT
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 15200
LENGTH: 1118
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Pred. No. 3.4e-35;
0; Mismatches 104; Indels 3
                                                                                                                                                                                                                                                                                                                                                   Length 1118;
                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_21066C.1
US-10-437-963-15200
                                                                                                                                                                                                                                                                                                                                                Score 181; DB 7;
Pred. No. 3.7e-38;
0; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               942 AAGGCAAGTTTCCTGTG 958
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                                                                                                                                                                                                                                                                                                                                                      7.3%;
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SEQ ID NO 27
LENGTH: 624
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                                                                                                                                                                                                                                                                                                                                                Query Match 7.3
Best Local Similarity 73.2
Matches 232; Conservative
                                                                                                                                                                                      TYPE: DNA ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Best Local 6
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Sequence 15200, Application US/10437963

Sequence 15200, Application US/10437963

Sequence 15200, Application US/10437963

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharow, Andrey A.

APPLICANT: Bribazuk, Brad

APPLICANT: Li, Ping

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Novel Carotenoid Hydroxylases for Use in Engineering Carotenoid
TITLE OF INVENTION: Metabolism in Plants
FILE REFERENCE: MSU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
SUPPRENT FILING DATE: 2004-01-02
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1007 TTGAGAGGGTTTGGTTGTTTTTTCAGATCGATGCATTGTGTAAGATAGTCCCGAGACAG 1066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        947 AAGTTTCCTGTGTTTTTTCTGTGGTTTGTTGATTGTGGAACAATTGGATTCTTGTTAA 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 GTGAAAGCTGAAAAGGCTGTAACTTTGATAAGGGAAACTGTTGAAGACCTTATTGCTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522 GGTGAGACGTCGATCAGTTGTACCATCTACACAAACGATTTCTCTCGGTGATGGTTGA 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      582 CAGAGITITITIGIAAATGIGCTGAGAGATTAGIGGAGAAGCTIGAGAACAICTGCITITAAG 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               818 -----AGATTGATTTGCTGTGCAAGATTCTTCTAGACAA 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    887 TTACACTGCTCTTAAAGAAGCTGAGCTTCGTTCTACTGATCTTCTGCCATATTGGAAGGC 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           853 ATAAAAGCAGAAAAGGCAGTTAACATCATCAGGAATACCGTTGAGGACCTAATTACCAAA 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                767 CGGAAGTGCTGTGAATATGGAAGCGAAGTTCTCTCAGATGACACTTGATGTCATTGGGTT 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GICTCTTTTTAACTACAATTTCGATTCTTTGACTACTGATAGTCCTGTCATTGAAGCTGT 886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     762 TTACACTGCACTCAAGGAAGCAGAACTTCGTTCTACAGATCTTTTACCATACTGGA----
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                                                                                                                                                                                                                                                                                                                                                                              Length 1686;
                                                                                                                                                                                                                                                                                                                                                                         Score 183; DB 9; Length 16 Pred. No. 1.3e-38; 0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.4%;
Best Local Similarity 61.8%;
Matches 363; Conservative
                                                                                                                                                                                                                                                                                         ORGANISM: Oryza sativa
US-10-751-235-22
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LENGTH: 1686
TYPE: DNA
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Sequence 26, Application US/10751235

Sequence 26, Application US/10751235

Publication No. US20050150002A1

GENERAL INFORMATION:
APPLICANT: DellaPenna, Dean
APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Necabolism in Plants
TITLE OF INVENTION: Metabolism in Plants
TITLE OF INVENTION: WASU-08604
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
CURRENT FILING DATE: 2004-01-02
SOFTWARE: Patentin version 3.2
SEQ. ID NOS: 744

SEQ. ID NO 26

SEQ. ID NO 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               811 TTGATGTCATTGGGTTGTCTCTTTTAACTACAATTTCGATTCTTTGACTACTGATAGTC
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                                                                                        GTATCCTGCGTTTCTTGCTTGCAAGCAGAAGAGGTTTAAAACTTTTTTCCTT 1249
                                                                                                                    392 GCATCCTTCGATTTTTGCTTGCTAGCCGTGAGGAGGAGTTTCAAGTTTACAACTT 444
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62.1%; Pred. No. 2.2e-28;
tive 0; Mismatches 94;
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Best Local Similarity 62.1:
Matches 300; Conservative
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US-10-751-235-26
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US-10-437-963-15203
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Sequence 25, Application US/20050150002A1
Sequence 25, Application No. US20050150002A1
Publication No. US20050150002A1
GENERAL INFORMATION:
APPLICANT: DellaPenna, Dean
APPLICANT: Tian, Li
APPLICANT: Kim, Joonyul
TITLE OF INVENTION: Metabolism in Plants
TITLE OF INVENTION: Metabolism in Plants
CURRENT APPLICATION NUMBER: US/10/751,235
CURRENT FILING DATE: 2004-01-02
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.2
SEQ ID NO 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1017 TTGGTTGTTTTTTCAGATCGATGCATTGTGTAAGATAGTCCCGAGACAGGTGAAAGCTG 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1137 TTGTCGAAAGAGAGAGAGAAAGAATCAATGATGAGGAGTATGTAAATGATGCTGACCCAA 1196
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                                                                                                                                                                                   847
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                                                                                                                             293
                                                                                                                                                                                                                  TCCATCACTTCACAAGAAGTACTTATCAGTAATAGTTGATCGTGTATTTTGCAAATGCTC 233
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                                                                                                                             234 cgagagectricicgaaaagcraagarcaracgcacgcagrgacacgccrcrcrraacargga
                                                                                                                                                                                                                                                                                               CGATTCTTTGACTACTGATAGTCCTGTCATTGAAGCTGTTTACACTGCTCTTAAAGAAGC
                                                                                                                                                                                                                                                                                                                               354 TGACTCACTTACGGCCGATAGTCCTGTAATTGAATCTGTTTATACCGCACTAAAAGAAGC
                                                                       AGAGAGGCTTGTTGAGAAGTTGCAGCCTTATGCAGAAGACGGAAGTGCTGTGAATATGGA
                                                                                                                                                                                   788 AGCGAAGTICTCTCAGATGACACTTGATGTCATTGGGTTGTCTTTTTAACTACAATTT
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Pred. No. 9.2e-33;
0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-751-235-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V Match 6.5%;
Local Similarity 61.7%;
les 329; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-10-751-235-25
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Best Local S:
Matches 329
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GENERAL INFORMATION:

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; OTHER INFORMATION: Clone ID: PAT_MRT4530_21069C.1
US-10-437-963-15203
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Job time : 1962 secs
Publication No. US20040123343A1
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ORGANISM: Oryza sativa
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Aeb16950 Green alg
Aeb16944 Rice Cyto
Abx56811 Arabidops
Aad681813 Cinnammat
Aeb16559 Diatom Cy
Ad41813 Cinnammat
Aeb16559 Diatom Cy
Ad41813 Cinnammat
Ad41250 Bacterial
Ad41298 Rice gene
Ad4057071 Tobacco c
Ad085139 Nicotiana
Adn37071 Tobacco c
Ad085135 Nicotiana
Ad11644 Nicotiana
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(pos:942. .1037, aa:Lys-Ile)
(pos:1242. .1326, aa:Val-Ser)
(pos:1420. .1223, aa:Lys-Asn)
(pos:1662. .1841, aa:Val-Leu)
(pos:1839. .2055, aa:Val-Trp)
(pos:2081. .2183, aa:Lys-Phe)
(pos:2340. .2440, aa:Asn-Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thale cress LUT1 (cytochrome P450 97C1) cDNA, SEQ ID NO: 5.
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1. 2467
4. *tag= a
/product= "Thale cress LUT1 protein"
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(TIAN/) TIAN L.
(KIMJ/) KIM J.
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     Aeb16909 Thale cre
Aeb16910 Thale cre
Aeb16911 Thale cre
Adt15447 Plant cDN
Adx61765 Plant ful
Aeb16926 Wheat cyt
Aeb16929 Barley cy
Aeb16929 Sunflower
Aeb16929 Tomato cy
Aeb16929 Maize cyt
Aeb16943 Thale cre
Aeb16943 Thale cre
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Score

Result

The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent entioxidants. The present sequence is thale cress LUT1 [cytochrome P450 monooxygenase (CYP97C1); AC3953130 genel CDNA. Note: The current sequence is that of thale cress LUT1 cDNA which is located on chromosome 3. New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds. Claim 10; SEQ ID NO 5; 135pp; English.

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Sequence 2467 BP; 657 A; 491 C; 521 G; 798 T; 0 U; 0 Other;

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New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotemoid production in a plant for enhancing production of specific carotemoid compounds.

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(TIAN/) TIAN L. (KIMJ/) KIM J. Dellapenna D, WPI; 2005-487984/49

Claim 10; SEQ ID NO 6; 135pp; English

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GTTGTTTGTTATTCCAAAGGTATGGGAAAAAGCTGAGGAATTTCTGCCTGAACGATTCGA
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                           GTCCATAGTATAACATAGGGGAGCCTAATCCTTCTTCTAATGATCTTTGTGTGGGTTCGG
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antioxidant; transgenic plant; chromosome 3.
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                                                          SEQ ID
                                                          LUT1 (cytochrome P450 97C1) DNA,
                                                                         engineering;
                                                                                                                                        02-JAN-2004; 2004US-00751235.
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                                                                       Pigment; metabolic engineeri
cytochrome P450 97C1; gene;
                                            (first entry)
                                                                                             Arabidopsis thaliana,
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                                            08-SEP-2005
                                                          Thale cress
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1741 GANGAGCTCANGTTCTTCTCTGGGAACTATAAGGTCAATACCGAACAAGAAC 2809   2750 GANGAGCTCANGTTCTTCTCTGGGGAACTATAAGGTCAATACCGAACAAGAAC 2809   2810 TTAYAGATTCAGTCTATAACCGGGAACAACACACACACACACAC	RESULT 3 ARB16911 ID ARB16911 standard; cDNA; 2467 BP.  XX AC AEB16911; XX DT 08-SEP-2005 (first entry) XX XX DX DX Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97C1; XX XX XX XX XX XX XX XX XX XX XX XX XX
1610   TCCANTCTTCTCTATTGGGCTTAGCTGATTTTTTACATAGGCGGGGCGCTAGAG   1669     661   CGGTGGTTCCATCGCTTCACAGGAGGTATTGTCGATTGTTGAGGAGGAGTATTCTCCA   129     672   CGGTGGTTCCATCGCTTCACAGGAGGTATTGTCGATAGTAGGAGGAGTATTCTCCA   172     673   AATGGCAGAGGCGTTCACAGAGGACTTCTCTCTCTTCTTCTCTCTC	1441 TACTTTGCTATGCTAGAAATTTACTTGGATGGGAGCTTCTCTGTTTTACCTCTT 1500 2450 TACTTTGCTATGCTAGAAATTTACTTGGATGGGAGCTTCTCTGTTTTACCTCTT 2509 1501 CAAATTCTCTATGTTCATGAACTCATCTGCATTAAGGAAAGAAGAAGAAGAAGTAGACA 1560 2510 CAAATTCTCTATGTTCATAGAACTCATCATCTGCATTAAAGGAAAGAAGAAAAATAGAA 2569 1561 GAGTGTTAGAAGGAAAACTCGTCTCGCATTAAAGGAAAGAAGAAAAATACATCA 2569 1561 GAGTGTTAGAAGGAAAACCCGGCTTTCGAGGATATAAAGGAATTGAAGTACATCACTC 1620 2570 GAGTGTTAGAAGGAAACCCGGCTTTCGAGGATATAAAGGAATTGAAGTACATCACTC 2629 1621 GTTGTATAAAAGGAAACCCGGCTTTCGAGGATATAAAGGAAGTACATCACTC 2629 1621 GTTGTATAAAAGGAAACCCGGCTTTCGAGGATATAAAGGAATCAAGCTCATC 2689 1681 TCTCTAATTATTCATGAACTAAATTTTCTAATTGATTGAT

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Q Sequence 2467 BP; 658 A; 491 C; 520 G; 798 T; 0 U; 0 Other;
Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2466; Conservative 0; Mismatches 1; Indels 0; Gaps

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US2004216190-A1 Viridiplantae.

28-OCT-2004

18-DEC-2003; 2003US-00739930. 28-APR-2003; 2003US-00424599. 28-APR-2003; 2003US-00425115.

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                                                               TTATGATTTCAGTCTATAACATCCATCGTTCTTCCGAGGTACAGTTCTCTCTTCTCTC
                                                                                                     GTCCATAGTATAACATAGGGGAGCCTAATCCTTCTTCTAATGATCTTTGTGTGGTTCGG
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Plant; 88; gene; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lighin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield;

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The invention relates a recombinant DNA construct comprising a polymucleotide having any of 5544 mucleotide sequences (CDNAs SED ID NO: 15-544) and encoding a polymeptide with any of 5544 maino acid sequences (SEQ ID NO: 545-11088). The CDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which capanism. Also included is a method of sequences is derived from with organism. Also included is a method of proteining a plant having an improved property, comprising transforming a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region of plant with a recombinant DNA construct comprising a promoter region of plant with a recombinant DNA construct comprising transformed to polypeptide associated with the property, and growing the transformed polypeptide associated with the property, and growing the transformed of plant property is selected from improving plant coll tolerance. for pathway, for improving plant tolerance to plant disease, for glactomannan production, for production of plant sprowth requilators, for increasing the rate of improving plant tolerance to herbicides, for increasing the rate of collerance to extreme osmotic conditions for increasing the rate of the collerance to extreme osmotic conditions, for increasing plant tolerance to extreme osmotic conditions, for increasing plant tolerance to extreme osmotic conditions, for increasing the rate of modifying seed protein yield and/or content, for modifying seed protein yield and/or content, for modifying seed protein to peats, for yield improvement by modification of carbohydrate, introgen or phosphorus use and/or uptake modifying seed protein by providing improved plant growth and also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and encode a plant transcription factor. The methods with improving plant tolerance to extreme osmotic and frought
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels 494;
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Best Local Similarity 73.2%; Pred. No. 1.1e-208;
Matches 1347; Conservative 0; Mismatches 0;
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                                                                                                                                              TGTAAAGAAATTGTCGAAAGAGAAGGCGAAAGAATCAATGATGAGGAGTATGTAAATGAT 1186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
-TTGTGCAAGATAATCCCAAGACAG
                                                             1067 GIGAAAGCIGAAAAGGCIGIAACIIITGAIAAGGGAAACIGIIGAAGACCIITAIIGCIAAG
                                                                                                   725 ATABABAGCAGAGAATGCGGTTACGATTATAAGGAACACTGTTGAAGAGGCTGATTATGAAG
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P-PSDB; AEB16920.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYP97C) cDNA.
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                                                                                                                                                                                                                                                                                                                                         New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454 CAAGGTATTTTGTAAATGTGCTGAGAGCTAATAGACAAACTTGAGCCATATGCTTTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                827 GTCTCTTTTAACTACAATTTCGATTCTTTGACTACTGATAGTCCTGTCATTGAAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  574 ATCATIGITCAACTACAATITTGATTCCTCACAACAGATAGTCCTGTCATTGATGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTACACTGCTCTTAAAGAAGCTGAGCTTCGTTCTACTGATCTTCTGCCATATTGGAAGGC
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Pred. No. 1.6e-42;
0; Mismatches 127; Indels 89;
                                                                                                                                                                                                                                                            χ;
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                                                                                                                                                                                                                                                               Cao
                                                                                                                                                                                                                                                               Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGTTTC------
                                                                                                                                                                                                                                                               Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 32608; 15pp; English.
                                                                                                                                                                                                                                                                 Kovalic DK,
              28-APR-2003; 2003US-00425114.
                                                       06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.9%;
Best Local Similarity 63.2%;
Matches 371; Conservative
                                                                                                                  LIU J.
ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                     WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                                                                                                                                          pests, for confeimproving yield.
                                                                                                                                                                                                                                                               Zhou Y,
                                                                                                                                                                                                                          CAO Y.
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                                                                                                                  (LIUJ/)
(ZHOU/)
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02-JAN-2004; 2004US-00751235. 02-JAN-2004; 2004US-00751235.

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                                                       706
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                                                                                                                                                                                                                                                                                                                      783
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                                                                                                               GAGAGTATTCTGCAAATGTGCAGAGGCTTGTTGAGAAGTTGCAGCCTTATGCAGAAGA 766
                                                                                                                                                                                                                                                                                                                                                                                                                                      ------CAGATCGATTGCTGTGCAAGATTGTTCCTAGACTGATTGTTCCTAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               820 ATAAAAGCGGAAAAAGCAGTTAACACAATAAGGAATACCGTTGAAGAGCTAATTACAAAA 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCAAGGCAATCGTAGATGCTGAAAATGAACAGATTGAGGGTGAAGAATATGTAAATGAG 939
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                                                                                    GGTGAGACGTAGAGCAGTTGTACCATCTACACAAAAGATTTCTCTCCAGTAATGGTCGA
                                                                                                                                                                                        609 TGGTGAACCTGTTAATATGGAAGCGAGGTTTTCTCAAAAGGAATGAGATTGGTTT
                                                                                                                                                                                                                                 GTCTCTTTTTAACTACAATTTCGATTCTTTGACTACTGATAGTCCTGTCATTGAAGCTGT
                                                                                                                                                                                                                                                         669 ATCCTTGTTCAACTACAACTTTGATTCCCTCACATCAGATAGTCCTGTTATTGATGCTGT
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                                                       647 GGCGAGGCGTAGAGCGGTGGTTCCATCGCTTCACAGGAGGTATTTGTCTGTGATTGTGGA
                                                                                                                                                                        CGGAAGTGCTGTGAATATGGAAGCGAAGTTCTCTCAGATGACACTTGATGTCATTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               995
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a //*tag= a //*produce P450 97C (CYP97C) pr //product= "Barley cytochrome P450 97C (CYP97C) pr //ranal except= (pos:1585. .1587, as:Xaa) /note= "Xaa may be any naturally occurring amino
 Length 1086;
                            89;
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytochrome P450 97C (CYP97C) cDNA, SEQ ID NO:
DB 14;
Score 187.2; DB 14;
Pred. No. 2.9e-40;
0; Mismatches 138;
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Hordeum vulgare; subsp. spontaneum
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Query Match
Best Local Similarity 61.9%;
Matches 369; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGAGACGTAGAGCAGTTGTACCATCTCTACAAAAGATTTCTCTCAGTAATGGTTGA 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             707 GAGAGTATTCTGCAAATGTGCAGAGAGGCTTGTTGAGAAGTTGCAGCCTTATGCAGAAGA 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  534 TAAAGTGTTTTGTAAATGTGCTGAGATTGGTGGAAAAGCTCGAGACATATGCTTTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTACACTGCTCTTAAAGAAGCTGAGCTTCGTTCTACTGATCTTCTGCCATATTGGAAGGC
                                                                                                                                                                                                                              New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCTCTTTTTAACTACAATTTCGATTCTTTGACTACTGATAGTCCTGTCATTGAAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1067 GTGAAAGCTGAAAAGGCTGTAACTTTGATAAGGGAAAACTGTTGAAGACCTTATTGCTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 187.2; DB 14; Length 1638;
Pred. No. 3.5e-40;
0; Mismatches 138; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                        antioxidants. The present sequence is barley cytochrome P450 monooxygenase (CYP97C) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1638 BP; 406 A; 403 C; 427 G; 401 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                Claim 10; SEQ ID NO 23; 135pp; English
                                                                                                                                                                                    BM816653, BU987393, CA023004
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Best Local Similarity 61.9<sup>3</sup>
Matches 369, Conservative
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                                                                                                                        Dellapenna D, Tian
                                                                                                                                                     WPI; 2005-487984/49.
P-PSDB; AEB16919.
                                                            DELLAPENNA
                                                                          (TIAN/) TIAN L.
(KIMJ/) KIM J.
                                                                                                                                                                                                    DDBJ; AV835803
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                                                                                                                                                                                                                                                                                           engineering; antioxidant; transgenic plant; CYP97C;
                                                                                                                                                                                                                                                                                                                             GTGAAAGCTGAAAAGGCTGTAACTTTGATAAGGGAAACTGTTGAAGACCTTATTGCTAAG
                    642 TGGCAAACCTGTAAATATGGAAGCAAGGTTCTCTCAAAAGGAATGACTTTAGATGTGATTGTTTT
                                                                                   CGGAAGTGCTGTGAATATGGAAGCGAAGTTCTCTCTCAGATGACACTTGATGTCATTGGGTT
                                                                GTCTCTTTTTAACTACAATTTCGATTCTTTGACTACTGATAGTCCTGTCATTGAAGCTGT
                                                                                                                                                  /*tag= a
/product= "Sunflower cytochrome P450 97C (CYP97C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGACCCAAGTATCCTGCGTTTCTTGCTTGCAAGCAGAGAAGAGGT 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sunflower cytochrome P450 97C (CYP97C) cDNA, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            partial /note= "No start and stop codons"
                                                                                                                                                                                                                                   Location/Qualifiers
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P-PSDB; AEB16923.
GENBANK; BQ971938.
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(TIAN/) TIAN L.
(KIMJ/) KIM J.
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                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .1686
/*tag= a /*tag= //product= "Rice cytochrome P450 97C2 (CYP97C2) protein"
                                                                                                                                                                                                                                                  Pigment; metabolic engineering; antioxidant; transgenic plant; CYP97C2; cytochrome P450 97C2; gene; 88.
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                                                                                                                                                                                                                      Rice cytochrome P450 97C2 (CYP97C2) cDNA, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.4%; Score 183; DB 14;
11.8%; Pred. No. 5e-39;
ve 0; Mismatches 135;
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                                                                                                                                                                                                                                                                                                       Oryza sativa; japonica cultivar-group.
                                                                                                                        BP.
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                                                                                                                          AEB16924 standard; cDNA; 1686
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Conservative
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Matches 363; Conserv
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DDBJ; AK065689.
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(KIMJ/) KIM J.
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                                                                                                                                                                                         08-SEP-2005
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02-JAN-2004; 2004US-00751235 02-JAN-2004; 2004US-00751235 Kim J;

'n

Dellapenna D, Tian WPI; 2005-487984/49

GENBANK; BG643819.

P-PSDB; AEB16921

(DELL/) DELLAPENNA

(KIMJ/) KIM J.

(TIAN)

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667
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                                                                                                                    The present invention relates to genes, proteins and methods comprising carotenoid monoxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for antioxidants. The present sequence is sunflower cytochrome P450 monooxygenase (CYP97C) cDNA.
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 New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotemoid production in a plant for enhancing production of specific carotemoid compounds.
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                                                                                                                                                                                                                                                                  Sequence 624 BP; 186 A; 110 C; 144 G; 184 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                              Pred. No. 1.5e-35;
0; Mismatches 104;
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                                                                                         Claim 10;
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                                                                                               991 ATTGGATTCTTGTTAATTGAGAGGGTTTGGTTGTTTTTTTCAGATCGATGCATTGTGTAA
                                                                                                                                 ----TTGTGCAA
                                                                                                                                                               1051 GATAGICCCGACACAGGTGAAAGGTGAAAAGGCTGTAACTTTTGATAAGGGAAACTGTTGA
                                                                                                                                                                                              216 garaarcccaagacagaraaaagcagagaargcggrracgarraraaggaacacrgrrga
                                                                                                                                                                                                                                                                                                                   931 TGCCATATTGGAAGGCAAGTTTCCTGTGTTTTTTCTGTGGTTTGTTGATGTGTGGAACA
                                                                                                                                                                                                                                                              276 AGAGCTGATTATGAAGTGTAAAGAAATAGTGGAAGCTGAAAATGAACAGATTGAGGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thale cress cytochrome P450 97A (CYP97A) DNA, SEQ ID NO: 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; SEQ ID NO 41; 135pp; English
                                                                   185 recentacrecaacerrecrire----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JAN-2004; 2004US-00751235.
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/*tag= a
/product= '
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GENBANK; AY058173.
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KIM J.
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(TIAN/) 7
(KIMJ/) 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTCAITGAAGCTGTTTACACTGCTCTAAAGAAGCTGAGCTTCGTTCTACTGATCTTC 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microoxyganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is maize cytochrome P450 monooxygenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
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                                                                                                                                                                                       metabolic engineering; antioxidant; transgenic plant; CYP97C;
                                                                                                                                                                                                                                                                                                                        (CYP97C) protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                        Maize cytochrome P450 97C (CYP97C) cDNA, SEQ ID NO: 26.
                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .531
/*tag= a
/product= "Maize cytochrome P450 97C
                                                                                                                                                                                                                                                                                                                                            partial note= "No start and stop codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94;
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62.1%; Pred. No. 9.4e-29;
iive 0; Mismatches 94
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                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim J;
                                                                                                                                                                                                             cytochrome P450 97C; gene; ss
                                                           AEB16928 standard; cDNA; 531
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Best Local Similarity 62.1
Matches 300; Conservative
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TIAN L.
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P-PSDB; AEB16922.
GENBANK; BE552887.
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(TIAN/) TIAN L.
(KIMJ/) KIM J.
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GENBANK; AY056446.

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                                                                                                                                                                                                                                                                                                                                                                              825 GGCAGTGTACACTGTTCTAAGAGAAGACAGAAGACAGAAGTGTTTCACCCTATTCCTGTTTG 884
The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is thale cress cytochrome P450 monooxygenase (CYP97A) DNA.
                                                                                                                                                                                                                                                                                  881 AGCTGTTTACACTGCTCTTAAAGAAGCTGAGCTTCGTTCTACTGATCTTCTGCCATATTG 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antioxidant; transgenic plant; CYP97A;
                                                                                                                                                                                                                                                          AGAAGACGGAAGTGCTGTGAATATGGAAGCGAAGTTCTCTCAGATGACACTTGATGTCAT
                                                                                                                                                                                                                                                                                                            TGGGTTGTCTCTTTTTAACTACAATTTCGATTCTTTGACTACTGATAGTCCTGTCATTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytochrome P450 97A (CYP97A) DNA, SEQ ID NO: 40.
                                                                                                                                                    Length 1788;
                                                                                                                         Sequence 1788 BP; 517 A; 344 C; 407 G; 520 T; 0 U; 0 Other;
                                                                                                                                                                             95; Indels
                                                                                                                                                  Score 91; DB 14;
Pred. No. 8.1e-14;
                                                                                                                                                                             0; Mismatches
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34. .1821
/*tag= a
/product= "Thale cres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEB16942 standard; DNA; 2057 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pigment; metabolic engineering cytochrome P450 97A; gene; da
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Best Local Similarity
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P-PSDB; AEB16935
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                                                                                                                     The present invention relates to genes, proteins and methods comprising carotemoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotemoid ratios in plants and microorganisms using LUT1 epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotemoid production in a plant for antioxidants. The present sequence is thale cress cytochrome P450 monooxygenase (CYP97A) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Soybean cytochrome P450 97A (CYP97A) protein"
                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      engineering; antioxidant; transgenic plant; CYP97A;
                          New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 858 GGCAGTGTACACTGTTCTAAGAGAAGCTGAAGACAGAAGTGTTTCACCTATTCCTGTTTG
                                                                                                                                                                                                                                                                                                                                     TGTGGAGAGAGTATTCTGCAAATGTGCAGAGGCTTGTTGAGAAGTTGCAGCCTTATGC
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                                                                                                                                                                                                                                                                            Score 91; DB 14; Length 2057; Pred. No. 8.7e-14;
                                                                                                                                                                                                                                                  Sequence 2057 BP; 615 A; 377 C; 457 G; 608 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soybean cytochrome P450 97A (CYP97A) cDNA, SEQ ID NO:
                                                                                                                                                                                                                                                                                                           95;
                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "No start codon"
                                                                                             Claim 10; SEQ ID NO 40; 135pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEB16947 standard; cDNA; 1278 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pigment; metabolic engineering cytochrome P450 97A; gene; BB.
                                                                                                                                                                                                                                                                            3.7%;
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Matches 148; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                     The present invention relates to genes, proteins and methods comprising carotenoid monooxygenases in the cytochrome P450 family. The invention also relates to altering carotenoid ratios in plants and microorganisms using Lurl epsilon-hydroxylases and/or CYP97A beta-hydroxylases. The invention is useful in altering the carotenoid production in a plant for enhancing production of specific carotenoid compounds that are potent antioxidants. The present sequence is soybean cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; call cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator;
                                                                                                                                                                                                   New expression vector comprising a nucleic acid sequence encoding a polypeptide having monooxygenase P450 activity, useful in altering the carotenoid production in a plant for enhancing production of specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        651 AGGCGTAGAGCGGTGGTTCCATCGCTTCACAGGAGGTATTTGTCTGTGATTGTGGAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 AGACGICGIGCIAIAGICCCAGCAIGCACAGAAGIAIGIAGCAGCIAIGAIIG---GC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 711 GTATTCTGCAAATGTGCAGAGGCTTGTTGAGAAGTTGCAGCCTTATGCAGAAGACGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         771 AGTGCTGTGAATATGGAAGCGAAGTTCTCTCAGATGACACTTGATGTCATTGGGTTGTCT
                                                                                                                                              GENBANK; BF425906, BF596805, AW704660, AW704625, BI470164, BQ296458,
BM892469, AI938600, AI938382, BU544173, BI471346, CD410775, BF598710,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTGTACTGAGAGAAGAAGATCGAAGTGTTGCTCCAATTCCAGTCTGGGAG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 59.2%; Pred. No. 7.8e-14;
Matches 174; Conservative 0; Mismatches 117; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1278 BP; 389 A; 247 C; 297 G; 345 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant full length insert polynucleotide seqid 1109.
                                                                                                                                                                                                                                                                              Claim 10; SEQ ID NO 45; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADO82389 standard; cDNA; 1078
    02-JAN-2004; 2004US-00751235
                                                                                         Kim
                                                                                                                                                                                                                                                                                                                                                                                                            monooxygenase (CYP97A) cDNA
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                                                                                         Tian L,
                                                                                                                                                                                                                                                   carotenoid compounds.
                                                                                                                      WPI; 2005-487984/49.
                             DELLAPENNA
TIAN L.
                                                                                                                                      P-PSDB; AEB16938
                                                                                         Dellapenna D,
                                                             KIM J.
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the electronic form from the US patent office at the polynucleotide sequence. The recombinant by the polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme semotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for producing galactomannan, increased resistance to plant disease, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stream of the sequence represents a plant full length insert content. This sequence represents a plant full length insert of the polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 adaadcaairaciedcactrocaetrotoriecadaadarocaratecaderiedcada 305
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yield; plant growth; plant development; seed oil; protein yield;
protein content; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1109; 15pp; English.
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05-NOV-2001; 2001US-00985678.
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Best Local Similarity 69.8
Matches 118; Conservative
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TABASKA J E.
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ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAO Y.
                                                                                                                 Unidentified.
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(SCRE/)
(TABA/)
(CAOY/)
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UCRPT01 0 Mdlv4-404 Arabidops

QGC20K13.

**О**НВ9С20.у

AJ486563 AJ432371

CW166683 104 575 08403827 CSAH-PNP1 08736606 8b31b06.y

CX529617 ALV 011A CX541939 813 GNF0BH CZ799589 OC\_Ba017

AV422798

Perfect score:

Seguence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGY INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
Filength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana Pull-length cDNA Complete sequence from clone GSLTFB642A07 of Flowers and buds of strain col-0 of Arabidopsis thallana (thale cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weisenbach, J. and Salanoubar, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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    (bases 1 to 1709)

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TTC; GSLT. CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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DR952300
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AUTHORS
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BH931006 cdi10g10.
BH584135 BCHAD9OTF
CD828034 BN25.0691
CCB89683 7-2-E02430
CD828321 BN25.070G
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Copyright (c) 1993 - 2006 Compugen Ltd.
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http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis. Location/Qualifiers

/organism="Arabidopsis thaliana" /mol\_type="mRNA"

source

FEATURES

CV886111 CK290930 BF096935

897

3322.8 3312.4 301.2 228.6 220.4 211.8 211.8 211.8 209.6 204.8 203.2

723.2 701.4 499 473 442 429.4 386.6 323

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Result Š DR923995 CX186676 BP827113

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CNSOASYJ 1664 bp mRNA linear HTC 06-FBB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB26ZE04 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
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Pred. No. 1e-200;
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/tissue_type="Flowers and bu-
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AV827314 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-13-P07 5', mRNA sequence.
#AV827314 GI:19869374
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Arabidopsis thaliana
Bubaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 616)
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                                                                                   CATGITITICAGGAATTATCCAAAGTACGCTAAAGGCTTAGTCGCTGAAGTCTCTGAATTT
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                         Score 701.4; DB 10;
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0; Mismatches 9;
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llarity 98.5%;
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E I (bases I to 736)

May, B.P. Simorowski, J., Arroyo, J.-M., Vaughn, M.W., Shen, R., McCombie, W.R. and Martienssen, R.A.

Arabidopsis genomic sequences flanking Ds enhancer and gene traps in transgenic lines
Unpublished (2004)

Contact: Martienssen RA

Cold Spring Harbor Laboratory
I Bungtown Rd., Cold Spring Harbor, NY 11724, USA

Tel: 516 367 3829

Fax: 516 367 3829

Email: martiens@cshl.org

This sequence flanks a Ds transposon carrying a gene trap in line GTB284 The transposon is located within At3953130.
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                                                                               ------AGAACTCTTCTGCATTAAGGAAAGGAAAGAAAGAATAT 1159
 TICIACITIGCIAIGCIAGAGAATITIACITGGAIGGAGCITCICIGITCICAITIACCI 1497
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/clone_lib="Arabidopsis thaliana Landsberg Ds insertion
lines"
                                                                                                                                         CTTCAAATTCTCTATGTTCATAGAACTCATCTGCATTAAGGAAAGCACAAGAAGAAGTAG
                                                                                                                        ACAGAGIGITAGAAGGAAGAAACCCGGCTTTCGAGGATATAAAAGGAGTTGAAGTACATCA
                                                                                                                                                                                    CTCGTTGTATAAACGAGTCAATGCGTCTTATCCTCATCCTCTGTAAGCAATCAAGCTC
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/organism="Arabidopsis thaliana"
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/ecotype="Landsberg erecta"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (thale cress)
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Location/Qualifiers
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CW839414
CW839414.1 GI:56095204
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SAIL_133_B07.v3 SAIL Collection Arabidopsis thaliana genomic clone SAIL_133_B07.v3, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                  Sessions, A., Burke, B., Presting, G., Aux, G., McElver, J., Patton, D., Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton, D., Ballis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B., Mizel, T., Katagiri, P., Glazebrook, J., Law, M. and Goff, S.A. A high-throughput Arabidopsis reverse genetics system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Sessions A Applied Trait Genetics Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Bmall: allen.sessions@syngenta.com
ABRC Stock Number CS806450; T-DNA left border flanking sequences or Syngenta Arabidopsis Insertion Library (SALL) lines are available through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
Class: TDNA tagged.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 977)
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/clone="SAIL 133 B07.v3"
/clone lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using
modified TAIL-PCR strategy"
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/mol_type="genomic DNA"
/ecotype="Columbia"
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Pred. No. 2.5e-115;
); Mismatches 20;
                                                                                                                                                                                                                                                   (thale cress)
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Matches 482; Conservative
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                                                                             and Shindsatk, and the second analysis of Arabidopsis full-length cDNA (2002b)
Lu Unpublished (2002)
Contact: Motodaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadaki Tunkuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-64359
Fax: 81-298-36-64359
Fax: 81-298-36-64359
Fax: 81-298-36-9060
Email: meski@crt.riken.go.jp
An Arabidopsis full-length CDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhOI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
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Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Onoo,Y., Sakurai,T., Carninci,P., Kawai,J., Itch,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
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/clone="RAFL09-13-P07"
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/dow stage="plants at various developmental stages from germination to mature seeds"
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/clone lib="RAFL9"
/note="Site_1: BamHI; Site_2: Sall; subjected to dehydration (1, 2, 5, 10, 4r) and cold (1, 2, 5, 10, hr) treatments"
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Pred. No. 2.2e-122;

    .616
    /organism="Arabidopsis thaliana"

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llarity 100.0%; Pred. No. 2.2
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BH931006 708 bp DNA linear GSS 01-OCT-2002 odil0g10.gl B.oleracea002 Brassica oleracea genomic, genomic survey sequence.
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Mukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida, II; Brassicales; Brassicaceae; Brassica.
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
                                                                                                                                                                                                                                                             Genome Sequencing Center
Washington University School of Medicine
Baail: submissions@watson.wustl.edu
Plate: odii0 row: g column: 10
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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryots, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryots; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II, Brassicales; Brassicaceae; Arabidopsis.

E. (Dassel 1 of 657)

S. Jakoby, M., Stracke, R., Soerensen, T.R. and Weisshaar, B.

Arabidopsis thaliana cDNA library enriched in transcription factors

Unpublished (2003)

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaa@mpiz-koeln.mpg.de

Insert Length: 657 Std Brro: 0.00

Plate: 7 row: L column: 14

Seq primer: T7R; CTAATACGACTCACTATAGGGA.
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/ Oul type="mRNA"
/ cultivar="At7"
/ db xref="dat1:59748"
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/ dc xref="mRDIZp768L1470"
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/ note="vector: pSPORTI; site 1: NotI primer adapter;
/ site 2: Sall primer adapter; RNA from cellculture (At7) 5
/ days after incoulation treated with 0.002 mM cycloheximid
/ for 2 h in the dark. Sequence submission managed by
/ RZPD/GABI-Primary database: http://gabi.rzpd.de. This
/ clone is available from RZPD; contact RZPD (clone@rzpd.de)
/ for further information."
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                                                                                                                                                                                                                                                                                                                  CB255014 657 bp mRNA linear EST 31-DEC-2004 54-E018363-019-007-L14-T7R MPIZ-ADIS-019 Arabidopsis thaliana CDNA clone MPIZp768L147Q 5-PRIME, mRNA sequence.
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                                       AACACTGATTTCAAGTAAACTCAGTAGAACACATCTTTTGACACAAACTGATGAATCAAG
                                                            Indels 152; Gaps
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larity 79.5%; Pred. No. 4.8e-107;
Conservative 0; Mismatches 10;
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/organism="Arabidopsis thaliana"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

[ (bases 1 to 570)
Ayelle,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Ayelle,M., Haas,B.J., Kumar,N., White,O.R., and Town,C.D.
Whole genome shorgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis General.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     624 GCTGAAGTCTGATTTTTTACATAGGCGAGGCGTAGAGCGGTGGTTCCATCGCTTCACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="TOLOODH3"
/db_xref="teaxon:3712"
/clone="BOHAD90"
/clone=lbe="BOHAD90"
/clone=lbe="BOHAD90"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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Pred. No. 3.6e-92;
0; Mismatches 89;
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                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive, Rockville, M
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided
Seg primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .570
/organism="Brassica oleracea"
                            GI:17836592
                                                                                                                                                                                                                                                                                                     Other_GSSs: BOHAD90TR
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Local Similarity 82.0%;
nes 475; Conservative
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                                                                 Brassica oleracea
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BH584135.1
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Seq primer: -28RPpOT reverse
Class: shotgun
High quality sequence start: 81
High quality sequence stop: 434.
Location/Qualifiers
1. 708
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO100DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
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                                                                                                                                                                                                                                                                                                                                                                                   Length 708;
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llarity 81.9%; Pred. No. 1.2e-103;
Conservative 0; Mismatches 101;
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Matches 525; Conserv
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Gaps

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72-8024301-021-023-P17-frev ADIS-MPIZ 021 Brassica napus CDNA clone MPIZD1022P1723Q, mRNA sequence.
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                                                                                                                       421 GCTAAAGGCTTAGTCGCTGAAGTCTCTGAATTTTCTATTTGGTTCGGGTTTCGCTATCGCT
361 ITCGTAATTGTGAGCGACCCAGCGATAGCTAAACATGTTTTGAGGAATTATCCAAAGTAC
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Fax: +49-521-106 6423
Email: bernd weisshaar@uni-bielefeld.de
Insert Length: 716 Std Error: 0.00
Plate: 23 row: P column: 17
Seq primer: frev.
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                                                                                                                                                                                                                                                   547
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                                                                                                                                                                                                                                                      GAGGGACCTCTTTGGACGG
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Brassica napus
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                                                                                                                                                                                                                                                                               CD828034 559 bp mRNA linear EST 10-JUL-2003 BN25.069103F020124 BN25 Brassica napus cDNA clone BN25069103, mRNA sequence.
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                 1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AAACCCAAACCCAAACTCGAGACCAATTCATCGAAATCCCAATCATGGGTCAGTCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACCTAAAACCAAAACCCAAA---ATCCGAGACCACGTCGTGGGTCAGCCCCGAT
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               ACTGITGAAGACCITAITGCTAAGTGTAAAGAAATTGTCGAAAGAGAAGGCGAAAGAATC
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Best Local Similarity 80.8%; Pred. No. 4.4e-75;
Matches 403; Conservative 0; Mismatches 90; Indels
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                               1163 AATGATGAGGAGTATGTAAATGATGCTGACCCAAGTATC 1201
                                                                                                                                                /organism="Brassica napus"
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/clone_lib="BN25"
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CD828034.1 GI:32509974
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Genoplante
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CD828299 627 bp mRNA linear EST 10-JUL-2003
BN25.070F19F020125 BN25 Brassica napus CDNA clone BN25070F19, mRNA
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  103 ATGGAGTCTTGTCTCTTTCTCCCAATCTCCCTTTTTTTTCTCGTCTCTTTCACTGCAAAG 162
                                                                                                                                                                                                                                                                                        CCAATCGCGAACGCGAAGCTCGACGATGTCGCTGATCTCCTCGGAGGTGCTCTTCTTA 297
                                                                                                                                                                                                                                                                                                                            340 ccaarceceaececeaaecresaceacercresaecrreseaecaecaecrerrerre 399
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    (bases 1 to 627)

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Contact: Genoplante
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Location/Qualifiers
                                                               163 TCCAAACCTTTTCCCTCTCCTAAACCCAGATTC---GTCTCCATCAAAAGCCTCCATAGAG
                                                                                                                                                GATTGGCTCACACCACTCACCTCGCACCATCACCTCGGGCCAAAACGACGATTCAGGTATA
                                                                                                                                                                                                                                                                                                                                                                                                     400 CCGCTCTACAAATGGATGAACGAGTACGGACCCATCTACCGTCTCGCCGCTGGTCTTCGT
                                                                                                                           AAACCCAAACCCAAACTCGAGACCAATTC---ATCGAAATCCCAATCATGGGTCAGTCCC
                                                                                                                                                                                                          GATTGGCTCACACACTCACTCGTACCCTTTCCTCAGGAAAAACGACGAGTCAGGTATA
                                                                                                                                                                                                                                                                                                                                                                       CCTCTCTACAAATGGATGAATGAGTACGGACCCATTTACCGTCTCGCTGCTGGTCCTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 AACTICGIGGIGGIGAGCGAICCAGCGAIIGCGAAACACGIICTCAGAAACIAICCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACGCTAAAAGGCTTAGTCGCTGAAGTCTCTGAATTTTCTATTTGGTTCGGGTTTCGCTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             520 TACGCCAAAGGGTTAGTCGCTGAAGTCTCCGAGTTCCTTTTCGGGTCGGGTTTTGCCATC
                                          CCTACGCGTCTTTTATCACCAAAACCCAAATTCACATTCTCCCATCAGATCCTCCATTGAG
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Tel: 33 1 69 47 54 00
Pax: 33 1 69 47 54 10
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/organism="Brassica napus"
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80.5%;
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Brassica napus
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Best Local Similarity
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                262 TGGCTCACGTCACTCGCACCATCACCTCGGGCGAAAACGACGATTCAGGTATACCA 321
148 TCCAAACCTTTTCCCTCTCTAAACCCAGATTC---GTCTCCATCAAAGCCTCCATTGAG 204
                                        AAACCCAAACCCAAACTCGAGACCAATTCATCGAAATCCCAAATCATGGGTCAGTCCCGAT 180
                                                               205 AAACCTAAAACCAAAACCCAAAACCCAA---ATCCGAGACCACGTCGTGGGTCAGCCCCGGT 261
                                                                                                                    181 TGGCTCACAACACTCACTCGTACCCTTTCCTCAGGAAAAACGACGAGTCAGGTATACCA 240
                                                                                                                                                                                                       241 ATCGCGAACGCGAAGCTCGACGATGTCGCTGATCTCCTCGGAGGTGCTCTTTTTTTACCT 300
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                                                                                                                                                                                                                                                                                      CTCTACAAATGGATGAATGAGTACGGACCCATTTACCGTCTCGCTGCTGGTCCTCGTAAT 360
                                                                                                                                                                                                                                                                                                                            382 CTCTACAAATGGATGAACGAGTACGACCCATCTACCGTCTCGCCGCTGGTCCTCGTAAC 441
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Unpublished (2003)
Contact: Genoplante
Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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CD828321.1 GI:32510261
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This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene Atgg55130.

Details on the protocols used for generation of the sequence are described in References 1.3. The sequences are generated at the WPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CO072553 858 bp mRNA linear EST 15-JUN-2004
GR_Ea31M14.r GR_Ea Gossypium raimondii cDNA clone GR_Ea31M14 3',
                                                                                                                                                                                                                                                                                                                                                                                                                   Anotes PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA from the PCR were directly sequenced to determine the genomic sequence flamking the insertion. T-DNA derived sequences were enewowed.
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Gossypium raimondii
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
roside; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 858)
                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-480D04-019791"
/clone="Lb="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 TAGAGAATTTACTTGGATGGGAGCTTCTCTGTTCTCATTTACTCTTTCAATTCTCTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 AAGAAACCCGGCTTTCGAGGATATAAAGGAGTTGAAGTACATCACTCGTTGTATAAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1634 GTCAATGCGTCTCTATCCTCATCCTGTAAGCAATCAAGCTCATCTCTTAATTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1514 TTGATAGAACTCATCTGCATTAAGGAAAGCACAAGAAGAAGAAGTAGACAGAGTTAGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGAAACCCGGCTTTCGAGGATATAAAGGAGTTGAAGTACATCACTCGTTGTATAAACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
4 (bases 1 to 310)
Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.
Direct Submission
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 301.2; DB 10; Length
Pred. No. 2.6e-69;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       /ecotype="Col-0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1754 TCCTGA 1759
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CO072553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX531442 310 bp DNA linear GSS 04-APR-2004 Arabidopsis thaliana T-DNA flanking sequence GK-480D04-019791,
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                                                                                                                                120
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                    CCAATCGCGAACGCGAAGCTCGACGATGTCGCTGATCTCCTCGGAGGTGCTCTCTTAA
                                                  CTTACTCTTCTCTTCACTGCAAAA
                                                                                     94 Argeagrerierererecaarerecererrerrere-rerererereaaag
                                                                                                                              AAACCCAAACCCAAACTCGAGACCAATTC---ATCGAAATCCCAATCATGGGTCAGTCCC
                                                                                                                                                                                                                                                  210 AAACCTAAACCTAAACCTAAACCTAAACCCAAATCCGAGACCACGTCGTGGGTCAGCCCC
                                                                                                                                                                                                                                                                                         GATTGGCTCACAACACTCACTCGTACCCTTTCCTCAGGAAAAAACGACGAGTCAGGTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTCTCTACAAATGGATGAATGAGTACGGACCCATTTACCGTCTCGCTGCTGGTCCTCGT
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              Gaps
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              7;
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              91; Indels
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                                                    ATGGAGTCTTCACTCTTTTCTCCATCTTCCTCTT
                0; Mismatches
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BX531442.1 GI:31408572
                  404; Conservative
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BX531442/c
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704 bp DNA linear GSS 25-JUL-2005
Ba Oryza coarctata genomic clone OC_Ba0031L17
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/clone="CC_Ba0031L17"
/tissue_type="leaves"
/dev stage="mature"
/lab_host="DHID8"
/clone="Nector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                              Oryza coarctata
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
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1 (Dasea 1 to 704)
Kim, H., Scollura, K., Missotski, M., Byrne, M., Stum, D., Smart, D.,
Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wing, R.

OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
ERABIL: rwing@genome.arizona.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTCTCTTTTTAACTACAATTTCGATTCTTTGACTACTGATAGTCCTGTCATTGAAGCTG
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0031 row: L column: 17
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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                                                                                                      OC_Ba0031L17.r OC_Ba Oryza
3', genomic survey sequence.
CZ710414
                                                                                                                                                                                                       CZ710414.1 GI:71116126
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 652 GGCGTAGAGCGGTGCTTCCATCGCTTCAGGAGGTATTTGTCTGTGATTGTGGAGAGG 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TATITITIGCAAATGIGCCGAGAGATTAGIAGAGAAACTGCAACCTTTIGCATTAGATGGCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CTGCCGTGAACATGGAAGAAAAGTTTTCTCAACTGACTCTTGATGTTATCGGTCTTCGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATTTAATTATAACTTCGATTCGTTGACAACCGATAGCCCTGTCATTGATGCAGTTTATA 240
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Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and
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                                           Wing, R. A.
Global assembly of Cotton BSTs
Global assembly of Cotton BSTs
Contact: Rood A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 625 9595
Fax: 520 621 1259
Email: rwingegenome.arizona.edu
Plate: 31 row: M column: 14.
Location/Qualifiers
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                                                                                TITLE
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Search completed: January 13, 2006, 07:12:27 Job time : 9664 secs

Sequence

Sequence

Sequence 39157, A Sequence 39157, A Sequence 39157, A Sequence 58824, A Sequence 45303, A Sequence 53376, A Sequence 53376, A Sequence 13396, A Sequence 13396, A Sequence 23, Appl Sequence 23, Appl Sequence 281, Appl Seque

63, App]

Sequence

Sequence Sequence Sequence Sequence

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2241 GCAATTGTGGCACTCGCGGTGTTTCTTCAGCGGTTAAACGTTGAGCTGGTTCCTGATCAG 2300
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APPLICANT: Myeth
APPLICANT: Mounts, William M
TITLE OP INVENTION: Probe 100 For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR PILING DATE: 2005-05-26
PRIOR FILING DATE: 2005-05-26
SOFTWARE: Patentin version 3.2
SEQ ID NO 6065

    Sequence 1969, Application US/11136527
    Publication No. US20050287570A1
    GENERAL INFORMATION:
    APPLICANT: Weth
    APPLICANT: Wouts, William M
    TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

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Pred. No. 0.13;
US-11-136-527-337

US-10-246-708-2

US-10-995-561-67874

US-11-136-527-7978

US-10-750-623-39157

US-10-750-185-38124

US-10-750-185-68124

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US-10-750-185-631376

US-10-750-185-631376

US-10-750-185-531376

US-11-136-527-3882

US-10-995-561-11396

US-11-136-527-7805

US-11-136-527-7805

US-11-136-527-7805

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 6065, Application US/11136527; Publication No. US20050287570A1; GENERAL INFORMATION:
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; ORGANISM: Rattus norvegicus
US-11-136-527-6065
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'cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

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'cgn2_6/ptodata/2/pubpna/DET_NEW_PUB.seq:*

'cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

'cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*

'cgn2_6/ptodata/2/pubpna/USI1_NEW_PUB.seq:*

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US-10-750-185-52067

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US-10-750-185-4215

US-10-750-623-42915

US-10-750-623-42915

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US-10-750-185-211

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US-10-750-185-2189

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; Sequence 3880, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Wounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR PILING DATE: 2005-06-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3880
; LENTH: 2118
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Sequence 12, Application US/11121086

Sequence 12, Splication OS/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.

TITLE OF INVENTION UCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REPERENCE: 09138.6000-000000
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Pred. No. 0.25;
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FILE REFERENCE: 031896-041000 (AM101086);
CURRENT APPLICATION NUMBER: US/11/136,527;
CURRENT FILING DATE: 2005-05-25;
FRIOR APPLICATION NUMBER: US 60/574,294;
PRIOR PILING DATE: 2005-05-26;
NUMBER OF SEQ ID NOS: 362830;
SOFTWARE: PetentIn version 3.2;
SOFTWARE: PetentIn version 3.2;
LENGTH: 1923
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Best Local Similarity 60.4%;
Matches 67; Conservative
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                                                                                                                                                                                             TYPE: DNA; CRGANISM: Rattus norvegicus US-11-136-527-1969
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR PELLOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patent In version 3.2
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13.1%; Pred. No. 0.67;
ive 13; Mismatches 139; Indels
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Pred. No. 9.1;
0; Mismatches 103;
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR PILING DATE: 2006-05-04
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
SOFTWARE: 119160
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Best Local Similarity 49.8%;
Matches 102; Conservative C
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Best Local Similarity 43.1%
Matches 115; Conservative
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US-11-121-086-12
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Squence 1583, Application US/11136527

Publication No. US2005028757041

GENERAL INFORMATION:

APPLICANT: Wyeth

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

TITLE OF INVENTION NUMBER: US/11/136,527

CURRENT APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR PILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Parent In version 3.2

LENGTH: 732
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US-10-750-185-52067
US-10-750-185-52067
Sequence 52067, Application US/10750185
Publication No. US20050260603A1
GENERAL INPORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: TERR, Richard
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIL100-2
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VERSION 3.1
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1138 TGTCGAAAGAGAGAGGCGAAAGAATCAA 1164
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                          702 TKTGHGAAWRRAAWAAAAAAAAAA 728
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Best Local Similarity 43.1%
Matches 115; Conservative
                                                                                                                            11-136-527-1583
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APPLICATION AND ADDRESSIN AND ADDRESSIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADDRESSIN AND ADDRESSIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADDRESSIN AND ADDRESSIN-LIKE
TITLE OF INVENTION: PROFISE IS OF STATEMENT APPLICATION NUMBER: US/11/052,554A
CURRENT APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR PILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
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Publication No. US20050287531A1

GRERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: MERR, Richard
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: MAITON Denis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
CURRENT FILING DATE: 2003-12-31
CURRENT FILING DATE: 2003-12-31
FRIOR PELING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE PARES PAREDILIN VERSION 3.1

SEQ ID NO 52067
LENGTH: 1872
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Pred. No. 3.2;
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1.5%; Score 38; DB 6
Best Local Similarity 57.6%; Pred. No. 3.2;
Matches 68; Conservative 0; Mismatches
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; LENGTH: 1872
; TYPE: DNA
; OCGANISM: Bovine 19866880381128
US-10-750-185-52067
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Matches 68; Conserv
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US-11-052-554A-475
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Best Local S:
Matches 91
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Sequence 7976, Application US/1113527

Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US 60/574,294

PRIOR FILING DATE: 2005-05-25

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 352830

SOFTWARE: PatentIn version 3.2

SEQ ID NO 7976
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                                                                                                                                                                                                                                      1.5%; Score 37.2; DB 7; Length 8709; S6.6%; Pred. No. 13; tive 0; Mismatches 53; Indels 0
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APPLICANT: KERK, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAILION-2
CURRENT APPLICATION NUMBER: US/10/750,185
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Pred. No. 3.6;
0; Mismatches 42;
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MAI GENONICS, INC.
APPLICANT: DeNISE, Sue K.
                                                                                                  TYPE: DNA
ORGANISM: Helicobacter pylori J99
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Best Local Similarity 59.6%;
Matches 62; Conservative
SOFTWARE: PatentIn version 3.3
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; ORGANISM: Rattus norvegicus
US-11-136-527-7976
                                                                                                                                                                                                                                                                                                                  69; Conservative
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 69; Conserva
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US-10-750-185-42915
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US-11-136-527-7976
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                                                                     8709
                                        SEQ ID NO 475
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                                                                     LENGTH:
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1183 TGATGCTGACCCAAGTATCCTGCGTTTCTTGCTTGCAAGCAGAAGAAGGTTTAAACTTT 1242
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TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REPERENCE: MMI1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 42915
LENGTH: 986
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Pred. No. 6.2;
0; Mismatches
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SEQ TWARE: Patentin version 3.1
SEQ ID NO 42915
LENGTH: 986
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Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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Similarity 50.0%;
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Matches 91, Conserv
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CRGANISM: Bovine
US-10-750-185-42915
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US-10-750-623-42915
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US-10-750-185-28428/c
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Publication No. US20050266560A1

GENERAL INPORMATION:
GENERAL INPORMATION:
FPLICANT: PREUSS, DAPHNE
FILE REPERENCE:
FILE REPERENCE:
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/11/117,187

CURRENT PILING DATE: 2005-04-28

PRIOR APPLICATION NUMBER: US/09/531,120

PRIOR PRILING DATE: 1999-03-17

PRIOR PILING DATE: 1999-03-18

FRIOR PILING DATE: 1999-03-18

NUMBER: OF SEQ ID NOS: 212

SEQ ID NO 211

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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SEQ ID NO 997
LENGTH: 711
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48.3%; Pred. No. 5.8;
tive 0; Mismatches 108; Indels
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; ORGANISM: Arabidopsis thaliana
US-11-117-187-211
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Best Local Similarity 55.6%;
Matches 70; Conservative
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ORGANISM: Artificial Sequence
PEATURE:
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Best Local Similarity 48.33
Matches 101; Conservative
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US-10-793-626-997
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960 TITITICIGIGGITIGITIGATIGIGGGAACAATIGGATICTIGITAATIGAGAGGGTITG 1019
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                                        484 TIAATAACTCTTCCTATAGCAATTTCAATGAGAATAACTAAAGGATTTAAACAATTAATA
2079 TCAAGTAAACTCAGTAGAACACATCTTTTGACACAAACTACTGAATCAAGATTAGTGGTT
                                                                                                                             2139 TTGATTAGGGAATTTAAAAGATGATTTTTTTTTTTCACCAGATTCATCCCATTCAGTGGA
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; Dublication No. US20050260603A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: RERE, Richard
APPLICANT: RESER, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: PANTIN, Dennis
APPLICANT: APPLICATION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
ITILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REPREBRUCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
FRIOR FILING DATE: 2002-12-31
FRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE PELLOR OF SEG 10 NOS: 64922
SOFTWARE PATENTINY VETSION 3.1
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Pred. No. 7.8;
0; Mismatches
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Job time : 689 secs
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; ORGANISM: Bovine 19866881662207
US-10-750-185-28428
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1.5%;
Best Local Similarity 54.0%;
Matches 74; Conservative (
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iuis bade plank (uspto)